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**FIGURE 48**

MGALIISGSSAGPVTQASLPPWGLSHGRCGFLLYMENTLCSHRTQSFSELSQSLMRPGFLQM  
PYISCAKLSKIWFPAKPCLLAFLEVFLLMSRLSLFSKMICFLFLSFLFPPHIYTHAS

**Important features of the protein:**

**Signal peptide:**

amino acids 1-41

**Transmembrane domain:**

amino acids 88-107

**Casein kinase II phosphorylation site.**

amino acids 47-50

**N-myristoylation site.**

amino acids 24-29

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**FIGURE 49**

GGCTTCTACAGTCCACAACCCACCAGGCCAGGCCAGCAGAATGAGCCAGTGAGTGCCGGGGCTCCCAAGTT  
 TGGCTGTTGCTATGACAACTGGCCACTGCAGCCGGTCTCTTTGGGGGAAGGCTGTGTGGGCGAGGCCAGCCATGC  
 TACCCGAGTGGGGTGGCTGCTGGCCAGTGCCCATGGCTCTTTGTGCAGACTGGGCTGCCCGTGGGTACTTGGTGTG  
 CTCTGTGGGCGAATATAACCGCTTTCTGGTATGGCGGTCGCATGGCAATGCCAATAACTTTGCCTCGGAGCAGA  
 GTGCATGAGCAGCTGCCAGGAGTCTCTCCATGGGCCCGCTGCTCCCGAGCTGGGGCTTCTGGAGAGGACACCA  
 CACGGATGGTGGCGGCAGCAGTCTGTGAGGCGAGCAGAACCCAGCCAGCACAGGACAGGGGCCCGGCTGCAGAG  
 AAAGCCCTGGCCCTTCTGGTGGTCTGTGGCGGCAGAGCAACAGCCCTGGGCCAGGGGAGCCCCCCACACCCAGGC  
 CTTTGGAGAATGGCCATGGGCGAGGAGCTTGGGTCCAGGGCCCTGGACTGGGTGGAGATGCCGGATCACAGC  
 GCCACCCCTCCACAGCTCCTCCTACAGATCTCATTCCCACCTCTCCAGGATTAGCTTGGCAGGTGTGGAGCCCT  
 CGTTGGTGCAGGCAGCCCTGGGGCAGTTGGTGGGCTCTCCTGCTCAGACGACACTGCCCCGGAATCCGAGGCTG  
 CCTGGCAGAAAGATGGCCAGCCCATCTCCTCTGACAGGCACAGGCTGCAGTTCGACGGATCCCTGATCATCCACC  
 CCCTGCAGGCAGAGGACCGGGGCCCTACAGCTGTGGCAGCACCCGCCAGGCCGCGACTCCCAAGAGATCCAAC  
 TCCGCAATTATAGGGGTGACATGGCCGTGCTGTCTGAGGCTGAGCTGAGCCGCTTCCCTCAGCCAGGGACCCAG  
 CTCAGGACTTTGGCCAAGCGGGGGCTGTGGGCCCTGGGGGCCATCCCTCTTTCACACCCACAGCCTGCAACA  
 GGCTGCGCTTTGGAACAGAACAGCCCGGGTGGTGGATGCCAGTCCAGGCCAGCGGATCCGGATGACCTGCCGTG  
 CCGAAGGCTTCCCGCCCCAGCCATCGAGTGGCAGAGAGATGGCGAGCTGTCTTCTCCAGACACCGAGCTGC  
 AGCTGATGGCTCCCTGGTCTATTAGCCGAGTGGCTGTAGAGATGGCGGCTTCTACACCTGTGTGCTTCAATG  
 GCGGAGACCGAGACCGAGTGGGTCCAGCTCAGAGTCTTGGGGAGAGCTGCAATCTCAGGACTGCCCTCACTG  
 TGACAGCTGTCAGAGGGTGATACAGCCAGCTAATTGTGTGGTAGCAGGAGAAAGTGGAAATCAGCAGGGTCCA  
 GGAACGGGCTACCTCTGTCAGGCTGTATGGCCACCGCTGTCCACCAAGTCCCAAGTGGCAGCTGCTCATTTACA  
 CTGGGGCCAGGAGTATAGGCTCTCATATGTGCAGTGCTTACCAGGGAGCCAGGAGCTCAGCCGAGCAGCCAGG  
 TGAAGGTGGTCTCACCAGCACCCACCGCCAGCCAGGGACCTGSCAGGAGCTGGCTCGACAGCCACAGAGCTGG  
 CCAACTGTGATTTGATCCTGCAGCCCAAGCTTTGTGGCAATGATATTATCCAGCTTCTGCTGTGGCAGCTGT  
 CACGTTTCCAGCTCAGCTCAGCCATCTGGCAGTAGGAGTGAAGGCTAGTTCTCAGCCCAAGTCCAAATAGTT  
 CATAGGCTAGGAGAAAGGAGATGGACTCTTGGCTTCCCTCTCTGGCTGGCAAGGAGTATTCTTCTGGAA  
 TACATTAGCTCTTTCAAAACCCACCCAGTGTTTAGCCTCAACGCGACCCAGTTACACCTTCTCTCTGTAGCTT  
 TCAGCAGTGTTCATCTCTGACATAACACAGGCTGCTGTTTCAAGAGAGCAATCTGTTGGATAAAGAAA  
 CCTTTACCTTTACAGCTTCCCTTTATAATTTGTTACACAGGAATAGTTAAATGCATTGTTTGTGTTTGTAG  
 ACGGAGTTTCACTCTTGTGGCCAGGCTGGAGGGCAATGGCGCGATCTCAGCTCAGTGCACCTCCGCTCTCTGG  
 GTTCTTGATTCCCTGTGTGACGCTTCTGAGTAGCTGGGATTACAGATGGCATCACCATGCCCTGGGTAAATTTT  
 GTATTTTGTAGTGGATGGGTTTTCGCCATGTTGGCCAGGCTGGTCTCGAAGTCTTGACCTCAGATGATCTGCCC  
 GCCTCAGCCTTCCCAAGTGTCTGGGATTACAGGCATGAGCCACACGCCAGCCATCAATGCATTTTTTTTATTTT  
 TTTTGTGAGACAGAGTTTCCGACTTCTTGGCCAGGCTGGAGTACAAATGGTGGCATCTTGGCTCAGCTCGAACCTCC  
 ACCCTCTGGGTTCAAGCCCTCTCCAGCCTCAGCTCCTGAGTAGCTGGGATTACAGGTATGTGCCACCATGCTT  
 GGCTAAATTTGTATTTTGTGGAGAGCGGGTTTCTCCATGTTGGTGCAGCTGGTCTTGAATCCCGACCTCAGG  
 TAAATCCGCGCCTCCGCTCCCAAAATGCTGGGATTAGAGGTCTGAGCAGCTGCCACGCCCATTAATGTGTT  
 TTAAGCTAGCTGTGACGGTTTCCACTTAATTTAAAGCTGGGCGAGGAGATGTGTAATGATTTCAAAGTTAACACC  
 TGTGTTGTTTCTAAAGGGCATGCCAAGTCTGCTGTATCAGGGAAGTATTCTGTGCTAAATCAGCGATGGTCTTA  
 TGTCTATGCTCTCTCACCCTCTCAGGCACTGAGCATCAGTCAGCTTAAATCTGGTGCAGAGGGTTACAGCAT  
 ACTTCTGTTGGCAAAATGGAATAGATGTTAAGACCTCAATAGGGATTGGGATGAACAGCTGCAAGTAGCATT  
 GCTTCTGAGCATGAAGAACTGGAAACGCTCCTTACGTGAGATCTTGGACCTTGAAGCCCTCTGAGGCGAAC  
 GTGCAAAATCTGGCTGTGACGGTTCATCTGACACCTGTGTAAAGCTGACCAAGCTGCTGTGTACAGTGACAAATGAG  
 GAGCCCTCTCTTCTTAAATGAGGAATCTGTGAAGCAAAATGTTTGTGCCAAAGACAAATCAGACTCAGCTGAGTGA  
 TTAATAAACAGCATATAGCAGGATGAGATAGCAATGGGGAAGGGTTGTGGGCAATGCAGTAACAGGGAATGGCTT  
 CAGAAATGGTTGAGTGTGGAAGACACATTTCTTCACTCTCAGGACTTCTAATTCCTTGTATGCTAAAGAGAGG  
 CATGGATTCTATGAGCTTCCAGTCCCTTTCCACTTTAACTTCTACAAATCTTTGAGGAGACTGCCCTAGTAGCA  
 AAGGTTATTCCTGGACAGGAAAGACGGGCATTACAGGAGCAAAAGCTCTGAAGGCTGACTTTTATTAACACA  
 CAGTGGTCCGAAAGGACAAACACATCAGGGTGAAGTACATCTCTGCTGCTCTCTTCTACTTCAACAAAGG  
 AAGTGTGGGCTGGGCGAGGCTCTTTTTCATTTAATACTGGAAATAATTAAGAGAGCATCATGTTCACTTAATG  
 CACTGGTTTGTCTATGAAATTTGAAATAAAGGCCACTTTTGTG

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**FIGURE 50**

MGPVVPVSLGLLEGAPTRMVAAAVLQASRNPASTGQGPRCRES PGLLVVSGGKTNLSLGQGRPPT  
PRPLENGHGGRSLGPGPLDWVEMPDHQRHPSTAPPTDLTSHLSRISLAGVEPSLVQAALGQLV  
RLSCSDDTAPESQAAWQKDGGQPISSDRHRLQFDGSLIIHPLQAEDAGTSCGSTRPGRDSQKI  
QLRIIGGDMAVLSEAELSRFQPRDPAQDFGQAGAAGPLGAIPSSHQPANRLRLDQNPV  
DASPGQIRIMTCRAEGFPPPAIEWQRDGGQFVSSPRHQLQPDGSLVISRVAVEDGGFYTCVAFN  
GQDRDQRWVQLRVLGELTISGLPPTVTVPEDTARLLCVVAGESVNIRWSRNLFPVQADGHRV  
HQS PDGTLIIYNLRARDEGSYMC SAYQGSQAVSRSTEVKVVSPAPTAQPRDPGRDCVDQPELA  
NCDLILQAQLCGNEYYSSECCASC SRFPHPAQPIWQ

**Important features of the protein:**

**Signal peptide:**

amino acids 1-16

**Tyrosine kinase phosphorylation site.**

amino acids 392-400

**N-myristoylation sites.**

amino acids 9-15, 50-56, 112-118, 146-152, 173-179, 195-201,  
220-226, 229-235, 280-286, 306-312, 336-342, 397-403

**Myelin P0 protein.**

amino acids 153-182

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**FIGURE 51**

CAGGCAGAAGCGAACAAAGACCCAGCAAGAGAAGGCAGAGGCTAAGACCCATCCCGTATCTGC  
TCTCCTGAAATAATTCTGGAGTCATGCCTGAAATGCCAGAGGACATGGAGCAGGAGGAAGTTA  
ACATCCCTAATAGGAGGGTTCTGGTTACTGGTGCCACTGGGCTTCTTGGCAGAGCTGTACACA  
AAGAATTTCAGCAGAATAATTGGCATGCAGTTGGCTGTGGTTTCAGAAAGACAAGACCAAAAT  
TTGAACAGGTTAATCTGTTGGATTCTAATGCAGTTCATCACATCATTTCATGATTTTCAGCCCC  
ATGTTATAGTACATTGTGCAGCAGAGAGAAGACCAGATGTTGTAGAAAATCAGCCAGATGCTG  
CCTCTCAACTTAATGTGGATGCTTCTGGGAATTTAGCAAAGGAAGCAGCTGCTGTTGGAGCAT  
TTCTCATCTACATTAGCTCAGATTATGTATTTGATGGAACAAATCCACCTTACAGAGAGGAAG  
ACATACCAGCTCCCTAAATTTGTATGGCAAAACAAAATTAGATGGAGAAAAGGCTGTCTGG  
AGAACAATCTAGGAGCTGCTGTTTTGAGGATTCCATTCTGTATGGGGAAGTTGAAAAGCTCG  
AAGAAAGTGCTGTGACTGTTATGTTTGATAAAGTGCAGTTCAGCAACAAGTCAGCAAAACATGG  
ATCACCTGGCAGCAGAGGTTCCCCACACATGTCAAAGATGTGGCCACTGTGTGCCGCAGCTAG  
CAGAGAAGAGAATGCTGGATCCATCAATTAAGGGAACCTTTCACTGGTCTGGCAATGAACAGA  
TGACTAAGTATGAAATGGCATGTGCAATTGCAGATGCCTTCAACCTCCCAGCAGTCACTTAA  
GACCTATTACTGACAGCCCTGTCTTAGGAGCACAAACGTCGAGAAAATGCTCAGCTTGACTGCT  
CCAAATTGGAGACCTTGGGCATTGGCCAACGAACACCATTTCGAATTGGAATCAAAGAATCAC  
TTTGGCCTTTCCCTCATTGACAAGAGATGGAGACAAACGGTCTTTTCATTAGTTTATTGTGTTG  
GGTTCTTTTTTTTTTAAATGAAAAGTATAGTATGTGGCACTTTTTAAAGAACAAAGGAAATA  
GTTTTGTATGAGTACTTTAATTGTGACTCTTAGGATCTTTCAGGTAATGATGCTCTTGCACT  
AGTGAAATTGTCTAAAGAACTAAAGGGCAGTCATGCCCTGTTTGCAGTAATTTTTCTTTTTTA  
TCATTTTGTTTGTCTGGCTAAACTTGGAGTTTGAGTATAGTAAATTATGATCCTTAAATATT  
TGAGAGTCAGGATGAAGCAGATCTGCTGTAGACTTTTCAGATGAAATTTGTTCAATTCTCGTAAC  
CTCCATATTTTCAGGATTTTTGAAGCTGTTGACCTTTTCATGTTGATTATTTTAAATTTGTGTG  
AAATAGTATAAAAATCATTGGTGTTTCAATTGCTTTGCTTGAGCTCAGATCAAAAATGTTTG  
AAGAAAGGAACCTTTATTTTTGCAAGTTACGTACAGTTTTTATGCTTGAGATATTTCAACATGT  
TATGTATATTGGAACCTTACAGCTTGATGCCTCCTGCTTTTATAGCAGTTTATGGGAGCAC  
TTGAAAGAGCGTGTGTACATGTATTTTTTTCTAGGCAACATTGAATGCAACGCTGATTTTT  
TTTAATATAAATATATAACTGTCCTTTTCATCCCATGTTGCCGCTAAGTGATATTTTCATATGT  
GTGGTTATACTCATAATAATGGGCCCTGTAAAGTCPTTTCAACCATTTCATGAATAATAATAAATA  
TGTAAGTCTGGCATGTAATGCTTAGTTTTCTGTATTTACTTCTTTTTTAAATGTAAGGACC  
AAACTTCTAACTAATTGTTCTTTTGTTGCTTTAATTTTTTAAAAATTACATTCTTCTGATGTA  
ACATGTGATACATACAAAAGAATATAGTTTAATATGTATTGAAATAAAACACAATAAAATTT

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**FIGURE 52**

MPEMPEDMEQEEVNI PNRRVLVTGATGLLGRAVHKEFQQNNWHAVGCGFRRARPKEQVNLLD  
SNAVHHIIHDFQPHVIVHCAAERRPDVVENQPDAAASQLNVDASGNLAKEAAVGAFLIYISSD  
YVFDGTPPYREEDI PAPLNLYGKTKLDGEKAVLENNLGAAVLRIPILYGEVEKLEESAVTVM  
FDKVQFSNKSANMDHWQQRFPHTVKDVATVCRQLAEKRMLDPSIKGTFHWSGNEQMTKYEMAC  
AIADAFNLPSSHLRPITDSPVLGAQRPRNAQLDCSKLETLGIGQRTPFRIKIKESLWPFLIDK  
RWRQTVFH

**Signal peptide:**

amino acids 1-30

**Transmembrane domain:**

amino acids 105-127

**N-glycosylation site.**

amino acids 197-201

**N-myristoylation site.**

amino acids 303-309

**Short-chain dehydrogenases/reductases family proteins.**

amino acids 18-30

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**FIGURE 53**

TGGGCTCCCTCCAGCACTGCTGTTGGCTGCTGCCTAAGATGGGTGACACTTGGGCCAGCTTCCCTGGCCTGGGC  
 CACCCACCCAGCAATGCTGCTGATCTCCCTCCTCTTGGCAGCCGGGTTGATGCATTCGGATGCGCGGCACCACTG  
 GCCCTGCTCTTTGCACTATGCCCTAAACAGGTGGTGGATTGTAGCAGCCAGGCGCTTATCTCGCTGCCCCAGAAC  
 TGGCAATGTGACACCGCAAAACCTCAGCTTGGCCACCAACCGCATCAGACGAGTGGCGCTGGCTACTTCATGCT  
 ACATGGAGCTCCAGGTCTGCTGATTTGGCACMACACTCCTTAATGGAGCTGCCCGGGGCTCTTCTCATGGCA  
 AGCGCTTGGCAGCACTTGGACCTGAGCTACAACAATTTACGCCATGTGCCAGCCGACATGTTCCAGGAGGGCCCATG  
 GGTAGTCCACATCGACCTGAGCCACCAACCCCTGGCTGGCGAGGGTGATCCCCAGGCGCTTTCAGGCGCTCATGAC  
 AGCTCCGAGACCTGGACCTCAGTTATGGGGGCTGGGCTTCTCAGCGCTGGAGGCTCTTGTAGGGGCTACCGGGGC  
 TGGTGACCTTCGAGATCGGTGGCAATCCCTGGGTGTGTGGCTGCAACATGGAAACCCCTGCTGAAGTGGCTGCGGAA  
 ACCGGATCCAGCGCTGTACAGCAAGATTCTCAGCTGGCTGAGTGCCGGGGGCCCTCTGAAGTGCAGGGGCCCCCGC  
 TCTTCTCAGTCACTGAGGAGAGCTTCAAGGCTGCCACCTGACCTGACCTGGATGATTACCTATTCAATTCGCT  
 TCGTGGGCTTGGTGTCTCATTTGCTTCTGTGGCCACCAACTTCTCTGGGCATCACTGCCAACTGCTGCCACC  
 GCTGGAGCAAGGCGAGTGAAGAGGAAGAGATTCAGCATGCTGCCCTCTCATCCCTCATGTGCTGCTGACCGCCACA  
 GCTGCTGGCCACCAAGCCCTCCCTGATTTGCTCACTGGTTCCATGGTGACCTGCTGCTCAGTCTATGTTGCTT  
 AAGCAAGGTGGGACACTCATTTTGTATGAGCATCTGCTTTGGGCCAGGCGGCCCTAGGAATTTGGGAACATCT  
 GATGAACCTGACTCAGCTCCCTGCCCTCAAGGCACITCCCTCTGGTCAAGGAGAGAGATCCAAAATATTCCCTTT  
 AAGACTATATGTACAGACTCTGAGCGCTCATTTATGGAGGCCAGAGGAGGCCATCATCTGTATTCAGCAATG  
 TCCATGAGAATTAATGATATGAGTGTATTGTGAATGGGTCACTAGGAATATCTACTTTGTCAAGTAGGCAAAA  
 GAGGGGTGTCTGCACATGGCAGAGGCCAGAAATGCAATGCTGTCTGTGTGAGAGAGTGAAGCAATCTCTGCTC  
 ACTTACTTGTATAGAGGGGGTGTGGCAGAGAATCAABCTACCCCTCAGCTCTGCACACCAAACTGTCAAGTCT  
 TCAGCAATCTGCCAGCCATGCCCTACAGGGAGTAAGAACACCTCTATGACAGCCCTGGCCCTCCTTCCACAGGAGC  
 TACCAGGTGAGACCCCTCCAGTGACTGCCCCATATGACCAAAATGTCAAGAGTGGTGAGGTCCTCCAGGACGCA  
 GCTGTGAGGTGTGACACTTTCAATGGCCTTGTCTGCTCCTCACTCAAGTTTGTCTCAGAGAGGAGGAGGAGGA  
 GGCCCAAGCAATCTGGGCGACGAGATCCTGGCACTTGGAGCCTAATCATGTGACTGTCTTCCGACCATGCTCT  
 ATGCCACAGGGTCTCAGCAGGAAGTGCAGTGTGGGCCACAGACCCAGCGCTGCAGACCCAGGAGCTAAAAGC  
 GGACAAAGGCGACGACATTTATGACCATATGAGGCTTTGCCATTTCTTCTAAGCAACTTACCACGTTAAGCATGA  
 GGTGTGAGAGAGCTATTAATTAATAAGCCCTTGCCAGCTTCAGGTACTTTGAAAAGCTCTTCGACCAAAACCATCTC  
 CTTTGACACACACACACAAATCTTTGAGTGAACGCTGTTGTTGCCATTTTCAGGATAGGCCAATAGAGCT  
 CAGAGAGGTTAAAGTCAGCTGCCACATGTAGCAAGATAAAGTCTGTGCTCTTCTACTGCCCCATCCAAGTGGG  
 GAACATCACCTTCCCTCAGAGTTATATAAATCAAACTAGAGCTGACAAAGTTCCCTCATAGAGTCCAG  
 GCACCTCCTTGGGCACTTTATATCTATGACTCACTTTTCAATTCTCACAGCAACTGCTGCTGTGTTTTT  
 ATTTATCCCATTTTCAGAGTGAATTAATCTGAGAGAGTTGAGTGACTTACCCAGGTTCTGTGGATAGCCCTAG  
 AAGGAGGGCGTAGGACGCTCCATCAGGGAATGCACTCAATCAGTCAGTCAAAAATCAAGTAACTTTACAGG  
 CAAGACCAATATTATCATCATCGGTGCTTCTTCATCAGTTTCTGTCAGCAGGATCAATATCTTCCCTCTATTGTT  
 CAGCAACCGATGCTTCATGACTATTTTGCATCTTCTCCTTGACTTTTCACTCCCTGTGCAGAGGTTAAATCA  
 AACATCAGTAACTGCTTTTACAGATGGGGAARAAAGTCAAGGTTGGATATGACTTGCATGTGGCAAGGTTG  
 GGGCTCAACCCCTAACACGTTTCTCTTCCAGTGCTTCTCAAGTGCTTGGGGAAGAGAAATGCCCTCAGAGGCTGG  
 GTAGTGGGGCCCTGGAATTCAGCATCCATGAATGTGCTAGTGGATGAATCAATTAAGAGGCGCAACCCATCT  
 GCTGTACAGATTGAACATATGCTCAGGTAGGGCAAAATGGAGGCTCTGAACAGAGACATACAGGTTAACCATGT  
 AATAGAGACCTCTGCTTTCAAGATGTGTAGATAAAACATCAGCAATGTGGCCATGTTGGGAGCTGATGTGAAAAG  
 TAGATCTTTGGGAATTAAGAAAGGAGACTGTGTTAAACACTCCCTGTCAGGCCCTGTGCGGTGTGTTGCAAGAG  
 ATACTAAGAGAGCAAGAAAGCTATAGGTGAGAACCTCTCGAGTTTAGGAGAGAAACATCAAGGACAGTCCCAACA  
 TGCTGATAAGTCTGGCCAGGAGGAGAAATTAACACAGGCTTTCACACCTCCCTTGCACCAGCTCCAGCGGTA  
 TTTCTTACGCCCATCTCTCTGAAAGCCCTGAAAGGAATGAGGAGGCTAATAGTCACTCTCAGGAGAGGCTCC  
 CTCACCTGTGCTTCCCTGAGCTCTCAACCAAAAGAGTCTTCAAAAACCTTGTGACCTGAGTACTTGAACCT  
 GTGTCCTCTGAATCTTTCTTACAACATCTGGGACAAATCCCTGGPCTGTGACATCCGAGCCAGACAGCTGTGCCCT  
 GCTCTCTCTCTGTGATGACCAAGAGTGGTGAATCAAGTGTGCTCTCAACGCCAGCCGACCAACCTTAATAC  
 TTGGAGAGGAACCTTTAGAAACTATATCTGCAAAAATGAAAAGTTTCCATAGGGGCAATACCATAATACTAT  
 AATAACCTCCAGGAACATATGTTTGGCCAAATGTAGTTAATATATTTTAAGATATATGCTTTTGTGATAGGAC  
 TAGAACCAAGAAAGACACCAATTTGCCCCCTTGACATCAATGTCCCTTTCTAGTGGGCAATTTGGTCTTAAT  
 GCCAAACCTTTCTGACAGGATACATGGCTTTAAAGGACAGATGTTTCTCTGCTGTGAGAGTTCTCTCAGTT  
 ACTAGGACCAATGAGGAAGATTTCAACCTCTGCGCAAGGAATTCCTGTCTTCCGCCACCGGCATCA  
 CTGCTTCCAGGCTATCAGAGAACCACTTCTAGAGATAATTAACAACTCTGATTAGAAATGCTCCCATATCCCTGG  
 TTGACCAAGGCTTCACTCAAAATGTCCAACTGGGTAACATGTATGTATGGGATCTCTCTGCTGTATGTGCT  
 GTCTGGAGGTTTCTTGTATTTGGCTGTCCGCTGACTTGGGACAGATCTCTCTAGAACTGGGTCAGTTCTCT  
 GACATGCTCCACTCAGCCATAGGCTGAGTGGCTAAATATGCAATAAAGCACTGCTAAATAGGCATATATAGGT  
 TGGTGAAGAAGTAATTTGGGTTTGGCCATTAAGATAGGCAAAAATCCCAATTAATTTTGGCTCAATCTAAT  
 ATTACATGCTTGTATAGATTAAGATGGAATCCCAACAGGTTTAGGGTAGGACTGGATGCTCAAAAAAATAA  
 AAAAAAATAAATAAATAAATAA

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**FIGURE 54**

MLLISILLAAAGLMHSDAGTSCPVLCTCRNQVVDCCSSQRLFSVPEDLPMDTRNLSLAHNRTAV  
PPGYLTCTYMEIQVLDLHNNSLMELPRGLFLHAKRLAHLDSLNNFNSHVPADMFQEAHGLVHID  
LSHNPWLRRVHPQAFQGLMQLRDLDSLGGGLAFLSLEALEGLPGLVTLQIGGNPWVCGCTMEP  
LLKWLNRNIQRCTADSQLAECRGPPEVEGAPLFSLTEESFKACHLTTLDDYLFIAFVGFFVS  
IASVATNFFLLGITANCCHRSKASEEEEEI

**Important features of the protein:****Signal peptide:**

amino acids 1-17

**Transmembrane domain:**

amino acids 241-260

**N-glycosylation sites.**

amino acids 52-55, 81-84, 107-110

**Tyrosine kinase phosphorylation site.**

amino acids 148-154

**N-myristoylation sites.**

amino acids 11-15, 263-268

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 175-185

**Leucine zipper pattern.**

amino acids 77-98

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**FIGURE 55**

GGCTGCGCCCAAGCGCGGGGCCAGCAGCTGCGAACCGCGGGCGCACACCTGTTTCCGCGC  
CCGGGGGACTTCCC CGCGCGGGGCTCAGAAAGTGTGGGTCGGTTCGCTTGCTTCCCCCTGGCGTCA  
GCGACCCAGGGTAACCTCCTCCACTGCTGCGTGCCGTGCAGGCCTGCCTGTGTGAGAGCCACG  
TGTGCCCGCTCTGGGCGACAGCCTTGGAAAGTCAGGACCGCGACGGGAGCAGAGCAGAAACCT  
TACAGAAACATGAAGCCCTCAACCATTCTGCTACTCAGTTATTTCGGGGCTGACGGCGGCTTCTA  
GAACATCCAGGTGTTCTGCAGATGCGAGAACTCATCCTGTAGTCACCAGATGGAGTCCCAAAC  
AGCCAAGCAGATGTAAGGCCTGTGCTGTGGCTCTGAGGCCCTGAATACAGAAGGGTCACTTTCT  
TAGTGGCCAAAGAGCAGTTGTTGACATTGATGTCTAATTATTGAACACGACGAGTCATTTTA  
CTGAGCTGCAGTGAGGAAACACTGACCATAGAAGATCAAGCCAAATGAGGGATTGCAAAATTC  
CTGATTCTTTTGAATTAGGATTCCAGATGGGGGCTCATTTCTACAGCCCCCAACATTCTTAT  
AGCCGTTATCACTGCCATCACCCTGCCACCAGCATCTTCTTGACAGATTCCACCCCTGCTCCC  
CAGAGACTTCTGCTTTGAAAGTGAGCAGAAAGGAAGCTCTCAGAAAAATCTCTAGTGGTGGC  
TGCCGTGCGTCCAGACAATCGGAATCCTGCCTTCAACCACATGGGCTGGCTTTTCTAAAGGT  
TTTGTGGCGGAGTGAGTTTCTCAGGATTCTTTATCCTCTTGTGGATTTTGTGATCAGTGG  
GAAAAACAGAGGACAGAACGCAAACTTTGTGATTATTTTGGCCGATGACATGGGGTGGGGTGA  
CCTGGGAGCAAACTGGGCGAGAACAAAGGACACTGCCAACCTTGATAAGATGGATGCTTGGAGGG  
AATGAGGTTTGTGGATTTCCATGCAGCTGCCCTCCACCTGCTCACCCTCCCGGGCTTCCCTTGCT  
CACCGGCGGCTTGGCCTTCGCAATGGAGTCACACGCAACTTTGCAGTCACTTCTGTGGGAGG  
CCTTCCGCTCAACGAGACACCTTGGCAGAGGTGCTGCAGCAGGCGGGTTACGTCAGTCACTGGGAT  
AATAGGCAAAATGGCATCTTGGACACCACGGCTCTTATCACCCEAACTTCCGTGGTTTGTGATTA  
CTACTTTGGAATCCCATATAGCCATGATATGGGCTGTACTGATACTCCAGGCTACAACCACCC  
TCCTTGTCCAGCGTGTCCACAGGGTGATGGACCATCAAGGAACCTTCAAAGAGACTGTTACAC  
TGACGTGGCCCTCCCTCTTTATGAAAACCTCAACATTGTGGAGCAGCCGGTGAACCTTGACAG  
CCTTGCCCAAGATATGCTGAGAAAGCAACCCAGTTCATCCAGCGTGCAAGCACCAGCGGAG  
GCCCTTCCTGCTCTATGTGGCTCTGGCCACATGCACGTGCCCTTACCTGTGACTCAGCTACC  
AGCAGCGCCACGGGGCAGAAGCCTGTATGGTGCAGGGCTCTGGGAGATGGACAGTCTGGTGGG  
CCAGATCAAGGACAAAGTTGACCACACAGTGAAGGAAAAACATTTCTCTGGTTTACAGGAGA  
CAATGGCCCGTGGGCTCAGAAGTGTGAGCTAGCGGGCAGTGTGGGTCCCTTCACTGGATTTTG  
GCAAACTCGTCAAGGGGGAAAGTCCAGCCAAGCAGACGACCTGGGAAGGAGGGCAACGGTCCCC  
AGCATTGGCTTACTTGGCTTGGCAGAGTTCCAGTTAATGTCAACAGCACTGCCCTTGTAAAGCGT  
GCTGGACATTTTCCAACTGTGGTAGCCCTGGCCAGGCCAGCTTACCTCAAGGACGGCGCTT  
TGATGGTGTGGAGCTCTCCGAGGTGCTCTTTGGCCGGTCAACGCTTGGGACAGGGTGTGCTGT  
CCACCCCAACAGCGGGGACGTGGAGAGTTTGGAGCCCTGACAGCTTCCGCTTGGAGCGTTA  
CAAGGCCCTTCTACATTACCGGTGGAGCCAGGGCGTGTGATGGGAGCATGGTGCCTGAGCTGCA  
GCATAAGTTTCTCTGATTTTCAACCTGGAAGACGATACCGCAGAAGCTGTGCCCCCTAGAAAG  
AGGTGGTGGGAGTACCAGGCTGTGCTGCCGAGGTACAGAAAGGTTTTCGACAGCTCCCTCCA  
AGACATTGCCAACGACAACATCTCCAGCGCAGATTACACTCAGGACCCCTCAGTAACCTCCCTG  
CTGATAGTCCCTACAAATTTGCCCTGCCCTGTCAAGCCGCAATACAGACCAATTTTATTCCAC  
GAGGAGGAGTACCTGGAAATTAGGCAAGTTTGGCTTCCAAATTTTACTTTTACCCCTTTACAA  
ACACACGCTTTAGTTTAGTCTTGGAGTTTAGTTTTGGAGTTAGCCTTGCATATCCCTTCTGTA  
TCCTGTCCCCCTCCACGCCACCCGAGAGCAGCTGAGCTGCCTGGCTCTGGGAGGAGGTG  
TGCTTAAATGGGAAGCACACGGCTTGGAGTCAGGCACAGGTGCCAGCTCCAGCTTTTGAAC  
TTGGGCAATTTGTTAACTTAACCTGCAAGTTGATTTTGGGGTTAAATAAAGGCATACATGAA  
AATGCTTGGCAACTTTAAAAA



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**FIGURE 56**

MGWLFLKVLLAGVSFSGFLYPLVDFCISGKTRGQKPNFVII LADDMGWGD LGANWAETKDTAN  
LDKMASEGMRFVDFHAAASTCSPSRASLLTGRLGLRNGVTRNFAVTSVGGLPLNETTLAEVLQ  
QAGYVTGIIGKWHLGHHGSHYPNFRGFDYYFGIPYSHDMGCTDTPGYNHPCCPACPQG DGPSR  
NLQRDCYTDVALPLYENLNIVEQP VNLSSLAQKYAEKATQFIQRASTSGRPFLLYVALAHMHV  
PLPVTQLPAAPRGRSLYGAGLWEMDSL VGQIKDKVDHTVKENTFLWFTGDNGPWAQKCELAGS  
VGPFTEGFWQTRQGGSPAKQTTWEGGHRVPALAYWPGRVPVNVTSALLSVLDIFPTVVALAQA  
SLPQGRRFDDGVDVSEVLFGRSQPGHRVLFHPNSGAAGEFGALQTVRLERYKAFYITGGARACD  
GSMVPELQHKFPLIFNLEDDTAEAVPLERGGAEYQAVLPEVRKVLADVLQDIANDNISSADYT  
QDPSVTPCCNPYQIACRCQAA

**Important features of the protein:****Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 353-373

**N-glycosylation sites.**

amino acids 117-120, 215-218, 356-359, 397-500

**N-myristoylation sites.**

amino acids 12-17, 33-38, 52-57, 97-102, 101-106, 113-118, 158-163, 328-333, 388-393, 418-423, 435-440, 436-441

**Amidation site.**

amino acids 382-385

**Sulfatases signature 2.**

amino acids 129-138

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**FIGURE 57**

TGGACAAGACACCTCCAGGAGCCAGCTCACAGCCACCGGTACCTTCTTCCAGGACAAGCTGG  
GGGCTCCATGGGCGCCTGAGGGCCAGGCGCCAGGGCCCTGGGCACGAGT**TAGG**TGAGACACC  
AGCCCTCGAGTACTACGAGCCACAGCTGTGGCTCTCCTGCCTCACGGGCATCTACGGCTGCC  
GTTGGAAAGCGTACCAGCGCTCCCATGATGATACACACCGGGCACAGCGCCATTCTCGCATG  
TGGGGGCTGTGGCAGCAGTACCATGCTCTCCTGGATCGTGGCAGGACAGTTTCGCCCCTGCAG  
AGCGGACCTCCTCCAGGTGACCATTCTCTGTACCTTCTTCACCGTGGTGTTGGCCCTTACC  
TGGCCCTCTCACCATCTCCTCTCCCTGCATCATGGAGAAGAAAGACCTCGGCCCAAGCCTG  
CTCTCATTGGCCACCGCGGGGCCCCATGCTGGCTCCAGAGCACACCGCTCATGTCTTCCGGA  
AGGCCCTCGAGCAGAAGCTGTACGGGCTCCAGGCTGACATTACCATCAGCCTGGACGGCGTGC  
CCTTCTCATGCATGACACCACCTGCGGGCGCACCAACCGTGGAGGAGGAGTTCCCGGAGC  
TGGCCCGCAGGCTGCCTCCATGCTTAACTGGACCACCTGACAGAGACTCAACGCTGGCCAGT  
GGTTCTTGAAGACTGACCCCTTCTGGACAGCCAGCTCCCTGTCAACCTCCGACCACAGAGAGG  
CCCAGAACCAGTCCATCTGCAGCCTGGCAGAGCTCCTGGAGCTGGCCAAGGGCAATGCCACAC  
TGCTGCTCAACCTGCGTGACCCGCCCCGGGAGCACCCCTACCGCAGCAGTTTATCAACGTGA  
CTCTGGAGGCGGCTGCTGCACCTCGGCTTCCCCAGCACCAGGTCATGTGGCTGCCCTAGCAGGC  
AGAGAGCCCTGGTGCGGAGGTTGGCTCCCGGCTTCCAAACAGCATCAGGCTCCAAGGAGGCAG  
TCGCCAGCCTGCGGAGAGGCCACATCCAGCGGCTGAACCTGCGCTACACTCAGGTGTCCCGCC  
AGGAGCTCAGGGACTACGCGTCTTGGAACTGTAGTGTGAACCTCTACACAGTCAACGCACCGT  
GGCTTCTCCTCCTGCTGTGGTGTGCGGGGGTCCCATCCGTCACTCTGACAACTCCACACCC  
TGTCCAGGTGCCCTTCCCCCTCTGGATCATGCCCGGACGAGTACTGTCTCATGTGGGTCA  
CTGCCGACCTGGTCTCCTTCAACCTCATCGTGGGCATCTTCGPGCTCCAGAAGTGGCGCTTG  
GTGGCATAACGGAGCTACAACCTGAGCAGATCATGCTGAGTGCTGCGGTGCGCCGGACACCC  
GGGACGTGAGCATCATGAAGGAGAAGCTTATTTTCTCAGAGATCAGCGATGGTGTAGAGGTCT  
CCGATGTGCTCTCCGATGTTTCAGACAACAGTTATGACACATATGCCAACAGCACCCGCCACC  
CTGTGGGCCCCGAGGGGGTGGCAGCCACACCAAGACCTCATAGAGCGGAGTGGGCGT**TAGC**  
TGAAGACATGTCTGTCCACCTGTACTGTACACAGAAGCTGGGGAGCCTAGGAGAGCTGGTGG  
AAGTGTGTCTGAAGTCTGGAGTGCTCTGGGAGCGGGCTCCACAGCCTCCTTGTGGGCTCCAGCC  
CCTTGTGAGCCGAGCCTCTCTTGAAGGGGACTCCCTGTCTCTGAGGCCAGCTGGGCCAGG  
ACTCCATCCTTTCAGATGCCCTGACAGGCTGGGGCTCCTTCTGGGAAGTATGGGGCCTAGGG  
CTTGGTCCCCCTTCTGAGGCCCTCTCCTGTATCCCGACCTGGAAGCTTTGATGGGTCTATGG  
GCCATGCCATACCCCTGTGGCAATGGAGTGTGTGGATGCTGCGCATCTGTGCTCTCCT  
GTCTGTGCCAGGAGGCACCTGAGTTCTCTGCTGTATCTGCCCAAGGGGCTGGGCCGAGGC  
TCTACCTGAAGCAACTCTGCTCTTCTGTGAGTCTCAAAGCACAAGAGGTTGAGCTCAGCCAGGAG  
GAAGCCAGTGTGCAATGTGGAGACACGTCTCTCCCAACCCACCTCATGCCACCGCCAAACCC  
CCTGCCCGAGGAGCGGGCTGAGCCACGTCCCTTAGGAGCAGCTGGAGATGGCCAAAAGAGTG  
AGCTCAGGACTACTGGATCCCATGTGCCAGTGTGCCAGACCTCAAGGCAGAAGGGTCACTT  
AACCAGGAGTCCACAGATGATGTGACCTCAGGTTCCACATCAGTGGCCACAGGGCAGGGC  
CCACCTGGTGAAGTGTCTGGATATGGCCAGGGTGGGTGTGTGGCTAAGTGGGCTGAACAG  
AGGGAACCTAGGGCCCTTGGCCAATGTGATTAAGCTGCCATCTTGAA

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**FIGURE 58**

MVRHQPLQYYEPQLCLSLCTGIYGCWKRYQRSHDDTTPGTAPFLHVGAVAAVTMLSWIVAGQ  
FARAERTSSQVTILCTFFTVVFALYLAPLTISSPCIMEKKDLGPKPALIGHRGAPMLAPEHTL  
MSFRKALEQKLYGLQADITISLDGVFPLMHDTTLRRTTNVEEEFPELARRFASMLNWTTLQRL  
NAGQWFLKTDFFWTASSLSPSDHREAQNQSICSLAEELLELAGKNATLLLNLRDPPREHPYRSS  
FINVTLEAVLHSGFPQHVMWLPSRQRPLVRKVAPGFQQTSGSKEAVASLRGHIQRLNLRYT  
QVSRQELRDYASWNLSVNLTYTNAPWLFSLWCAGVPSVTSDNSHTLSQVPSPLWIMPPDEYC  
LMWVTADLVSFLLIVGIFVLQKWRLGGIRSYNPEQIMLSAAVRRTSRDVSIMKEKLIFSEISD  
GVEVSDVLSVCSDNSYDTYANSTATPVGPRGGGSHTKTLIERSGR

**Important features of the protein:****Signal peptide:**

amino acids 1-24

**Transmembrane domains:**

amino acids 47-61, 77-93, 335-350, 380-399

**N-glycosylation sites.**

amino acids 182-186, 217-221, 233-237, 255-259, 329-333, 462-466

**Tyrosine kinase phosphorylation site.**

amino acids 130-139

**N-myristoylation sites.**

amino acids 21-27, 48-54, 294-300, 404-410, 442-448, 473-479

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**FIGURE 59**

CCTGAGCAAAACACAGCAGCCCGAGTGTTCCTCCAAAGGCCAAATAGCTGAGAACGTCCACTCTCTAA  
TCTGTGTGGTGGTCTGCATTGCCGGGGCCCCCTGGCTCTCTTCTGGCATTCTCTGCCTCTGGCT  
CATATTCTTGTAGGCCAGGTGGGCTTGCTCGAGGGACACCCCCAGTGCCTGGATTACGGGGC  
CCCTTTCCAGCCCTCTGCACCTTGAGTTTGTCTGACTATGAGTCTCTGGCTGCTGTGA  
TCAGCACAAGGACCGCCGCATCGCTGCCCGTACTGGGACATCATGGAATATTTTGATCTGAA  
GAGACATGAGCTGTGTGGAGATTACATTAAGACATCCTTTGCCAGGAGTCTCGCCCTACGC  
AGCCCACTCTACGACGCCGAAAAACACCCAGACGCCTCTCCGGAATCTCCGGGCTCTGCTC  
TGATTACTGCTCTGCCTTCCATTCTAACTGTCACCTCAGCCATTTCCCTGCTGACCAATGACCG  
CGCCCTCCAGGAGTCTCATGGAAGGGGACGGTACCCGCTTCTGCCACCTCCTGGACCTTCTCTGA  
CAAGGACTATTGCTTCCCTAATGTCTGAGGAACGACTATCTCAACCGCCACCTGGGCATGGT  
GGCCCAAGATCCTCAGGGCTGCCTGCAGCTCTGCCTGAGCGAGGTGGCCAACGGGCTGAGGAA  
CCCCGTCTCCATGGTCCATGCTGGGGACGGCACCCTATCGCTTCTTTGTTGCCGAGCAGGTAGG  
AGTGGTGTGGGTCTACCTCCCTGATGGGAGTCGCCTGGAGCAACCCCTCCTGGACCTCAAGAA  
CATCGTGTGGTACCACCCCATGGATCGGGGATGAGAGAGGCTTCTTGGGGTGGCTTTTACCC  
CAAATTCCGGCCACAATCGCAAGTTCTATATTTATTATTTCGTGCCTGGACAAGAAGAAGGTAGA  
AAAGTCCGAATTAGTGTGAGATGAAGTTTCTCGGGCTGATCCTTAACAAAGCTGACCTGAATC  
AGAGAGGGTCTCTTGGAGATTGAAGAACCAGCCTCAAACCATATGGCGGACAACCTCTTTT  
TGGCTTGGATGGCTATATGTACATATTCACGTGGGACGGGGACAGGCTGGAGATCCCTTTGG  
CCTGTTTGGAAATGCTCAGAACAAAAGTTCCCTGCTGGGAAAAGTTTAAAGGATCGATGTGAA  
CAGGGCAGGCTCAGATGGCAAGCGGTACCGAGTCCCTCGGACAATCCATTGTGTTCTGAGCC  
AGGGGCCCCACCCGCCATCTATGCCTATGGGATCAGGAACATGTGGCGTTGTCGTGTGGACCG  
AGGGGACCCCATCAGCGGCCAGGGCCGAGGCCGGATATTCTGTGGGGACGTGGGCCAGAACAG  
GTTTGAAGAGGTTGACCTCATTGTTGAAGGTTGGAACACTATGGCTGGAGAGCAAGGAAGGGTT  
TGCATGTTATGACAAAAAAGTTTGTGCAATGCCTCTTTGGATGATGTTCTGCCAATCTATGC  
TTATGGCCATGCACTGGGGAAGTCACTGAGTCACTGGAGGTTATGTCATCTGTTGTTGAATCCCC  
AAATCTCAATGGCCTGTATATCTTTGGAGACTTCATGAGTGGTGCATCTATGGCTTTGCAGGA  
AGATAGAAAAACAAGAAATGGAAGAAGCAGGATCTTTGCCTGGGCAGCACCAGCTCCTGTGC  
CTTCCAGGCTGATCAGCACCCATAGCAAGTTTCATCATCTCCTTTGCTGAAGATGAAGCAGG  
GGAGCTGTATTTCTGGCGACCTCTTACCACAAGTGCCTATGCACCACTGGATCTATTTACAA  
GTTTGTGTTACCCCTCAAGGCGAGCACCCAGGCAAGTGCAATACAAGCCAGTGGCCGTGAG  
ACCAAGAGTAAGCGGATCCCGTTACAGCACTCGCCAAGCAGTCTTGGACTTGCTAAAGGA  
ACAATCAGAGAAAGCTGCTAGAAAAATCTTCCAGTGCAACCTTAGCTTCTGGCCAGCCCCAGG  
TTTGTCTGAGAAAGGCTCCTCAAAGAAGCTGGCTTCTCCTACAGCAGCAAGAATACATCTGCG  
AGGGCTGGTACAAAGAAGAGCCAGAGTGGGGCCCCACGTCGCCAGGGCAAGAGGAGGAA  
GAGCCTGAAAGCCACATGGCAGGATGAGGCCATCAGCAGAGCAGAGCGAGCTGGCAGAA  
TCTCCCTTGAACCTATTGCTCAAGGTGGCCGACAGGTGACGTGAGAGAGGAGGCCACCTCAT  
CAAATGAAAGTCACTGCTGAATAAGACCTTAGAAGTCTGGGAAGCCAGGGTAGAGGTGGGGC  
AGGGCGGTTTCTCTCTCCCTGGGAAATCTTGCTGTCTACTGAATAAATAATGCACCTTCTCT  
GTATGCACTGCTCTGTGTGGGAGACCATATCCAGATTGCTGGTGCACCTGGGTTATGGTAAGC  
ACTAGTCCATGAGCCTGCTTGAATCAGCTGGATGTCTCCGTTTGTCTTGAATAGCTAC  
AACCTGAGGTAATAAATCAACATTTGCTCA

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**FIGURE 60**

MLRTSTPNLCGGLHCRAPWLSSGILCLCLIFLLGQVGLLQGHQPCLDYGPPFPPLHLEFCSD  
YESFGCCDQHKDRRIAARYWDIMEYFDLKRHELCDGYIKDILCQECSPYAAHLYDAENTQTPL  
RNLPLGLCSDYCSAFHSNCHSAISLLTNDRLQESHGRDGRFCHLLDLDPDKDYCFPNVLRNDY  
LNRHLGMVAQDPQGCLQLCLSEVANGLRNPVSMVHAGDGTTHRFVVAEQVGWVWVYLEDGSRLE  
QPFLLDLKNIVLTTPWIGDERGFLGLAFHPKFRHNRKFYIYSCLDKKKVEKIRISEMKVSRAD  
PNKADLKSERVILEIEEPASNNHGGQLFLGLDGYMIFTGDGGQAGDPFGLFGNAQNKSSLLG  
KVLRIDVNRAGSHGKRYRVPSDNPFVSEPGAHPAIYAYGIRNMWRCAVDRGDPITRQGRGRIF  
CGDVGQNRFEEDLILKGGNYGWRAKEGFACYDKKLCHNASLDDVLPYAYGHAVGKSVTGGY  
VYRGCESPNLNGLYIFGDFMSGRLMALQEDRKNKKWKKQDLCLGTTSCAFFGLISTHSKFII  
SFAEDEAGELYFLATSYPSAYAPRGSYKVFVDPSSRAPPGKCKYKPVVVRTKSKRIPFRPLAK  
TVLDLLEQSEKAARKSSATLASGAQGLSEKSSKKLASPTSSKNTLRGPGTKKKARVGPH  
VRQGKRRKSLKSHSGMRPSEAEQKRAGRSLP

**Important features of the protein:****Signal peptide:**

amino acids 1-41

**Transmembrane domain:**

amino acids 17-36

**N-glycosylation sites.**

amino acids 372-376, 480-484

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 645-649, 699-703

**Tyrosine kinase phosphorylation site.**

amino acids 81-89

**N-myristoylation sites.**amino acids 11-17, 37-43, 156-162, 165-171, 357-363, 365-371,  
368-374, 408-414, 459-465, 548-554, 557-563**Amidation sites.**

amino acids 391-395, 696-700

**Cell attachment sequence.**

amino acids 428-431

**Leucine zipper pattern.**

amino acids 25-47

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**FIGURE 61**

CTCCATTAAACCACCACCAGCTCCCCAAGCCACCCCTTCAGCCATGAGGTTCCCTGCTCCTGGT  
CTTGGCAGCCCTCGGATTCTTGACCCAGGTGATCCCAGCCAGTGCAGGTGGGTCAAAATGTGT  
GAGTAACACCCCAGGATACTGCAGGACATGTTGCCACTGGGGGGAGACAGCATTTGTCATGTG  
CAACGCTTCCAGAAAATGCTGCATCAGCTACTCCTTCTGCCCAGGCTGACCTACCACAGCT  
CATCGGTAACCCTGGCAATCAAGGAGAAGAAACACACAAGGAAAGACAAGAAGCAACAAAC  
GACCGTAACATCATATAAACCCTGCTATCGCCTCCACCAACTCAGAGAAATATCATTTCAC  
AGTTCCAATTCTCTACATTGCTGAGTACTAGCCAAGGCTCCTCTTTATGGGGCAGATATCT  
ATAGCCAACCCCAAACTTCTGTCTTCTATCATTCTGTCAATTCATCTAGTAACTAATTTGGAG  
TTTGTATCTATCTTACGAGAACAATCATCATGCAGATTGCTCCACAGGGGATCTGTCAAGTTG  
GGTCTCCAAATGAAAAATGTCAAGACAGAATTGGACATGCAAAAGATTGACTGGGAGAACAC  
ACCTCTGATGGACAAAGGTGAGACAGAGCAGCCACAGGCAGGGAGAGCCTTCAGACTGCAACG  
CTGGCCTGATACGTGTCAAAGGAGAGAGGGATAGAGGAGGATTGAATAGAAGGAGACTAAGAC  
TGCAGCTCTAAGAAAGTCTCAGCCAAACAGATGGGGAGGCCAAAGCAAGGCTTGCCCTCAG  
AGGAGCTCACGCAGGGCAGGAATAGCCAGGTTCTCATATCCAGGGGTTCAAGACTTGGCTGAG  
AACAGCCCTTGGAGAACATGGGGTGACTGCTACCATAGGTCTGGAAGTATGAGGCTGTCCACC  
AACTATCCCTTGAAGCAAGTTCTCTTGAAGGAAATCTAAACAGTGCACCCCATGCGCTGCC  
ACGGAGTATAAGGAGGGAGAGAAAGGAGCTGAAAGTCTAGGTTTGGCCAGCTAGGTAGACTGA  
CTTGTGAGGTATTTATTTATTCATTGTAGTAACAAGCAGACAGAATACATAGCCACCATTGG  
TAGTACACCCCAAAGCAAGGATGGCATGATGCTGGTGACTCAAACGTGCCTACTCATGGTGT  
CAAATTGGCATAATCCTCTTGGGAAGCTGTGTGGAAATAAGCACAGAGAAGCAGAAGCTAAT  
TGCTTAATCCACTAAACATTACTTCTGGGAATTGGCTCATATAAATTATCCAAGAGAAAGCA  
CAAAGTTATGGGCACAAAGGTTTCCATATAATATTATTTAAATGCTGAGAAAAATGAAAAA  
TCTAAATGGTGAAATATATACTAATGCCATCTATAAATACAAACAAATAGAATGTTTATAGAA  
TAATGGAACATAATAACATTATTCAAAATTGCATTTATGCTATAGTTGTCAAATTTGCTCCT  
TATATGATACAAAACCTCATGAAAATTATGACTTTTTTGTGGTTGGAAAGCAGAATTATGCA  
TAAATTTCTCTTACAGTTCGATGCCCATTAGTTTTATATAACATTTATTTGACACGCTACTGA  
CTTCTATCTGAGAAGAACAACCAAAACACTCAGGCCTAAATAATTAACACGGTCTCAAAA  
CTAGCAAACCAGATAAGAAAAGATGTTAATGCCCATTCCTTAACCTTATGTCTTAGACCAAAAT  
TAATTCATAGATGGTTTAAAAATGACAGGTGAAAAGTAAAGTATTAAGAAATTGTGGTCAAA  
TATTCAATTTAAGAGCAAGGAAATCTTATAAATATAACAATAGAGGCAGAACTCATGTAAGA  
ATAAATTGATTAGGTGGTATTAATATTAAGTTCCTATGTATGTCAAAGATATCATTTTGAA  
ATTCATCCATCTTATTGGGTATTGCAGGAGTTCATTCCCTTTTGTGTTATAAATACTCTTCCGT  
CATATGAATAGTATTCATTGTATACCTGGTTGTGTGATGGACATTTGGGTTGTTCCCGATTA  
TGGCTATTACAAATAAAGCTTCTATGAACATTTATGTACA

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**FIGURE 62**

MKELLVLVLAALGFLTQVIPASAGGSKCVSNTPGYCRTCCHWGETALFMCNASRKCCISYSFLP  
KPDLPQLIGNHWQSRRRNTQRKDKKQQTTVTS

**Important features of the protein:****Signal peptide:**

amino acids 1-16

**Transmembrane domain:**

amino acids 1-22

**N-glycosylation site.**

amino acids 50-53

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 79-82

**N-myristoylation site.**

amino acids 23-28

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**FIGURE 63**

GCGGAGCGCCTGGGAGAGGAGAAGGAGCCGACCTGCCGAGATGCGAGGCGACCGGCACCTGGGC  
GCTGCTGCTGGCGCTGGCGCTGCTCCTGCTGCTGACGCTGGCGCTGTCCGGGACCAGGGCCCCG  
AGGCCACCTGCCCGCCGGGCCACGCCGCTACCACTGCTGGGAAACCTCCTCGAGCTACGGCC  
CGGGGGCGCTGATTTCAGGGCTCATGCGGCTGAGTAAGAAGTACGGACCGGTGTTCCACATCTA  
CCTGGGACCCCTGGCGGCTGTGGTGGTCTGGTGGGACGAGGCTGTGCGGGAGGCCCTGGG  
AGGTACGGCTGAGGAGTTTCAGCGGCCGGGGAACCGTAGCGATGCTGGGAAGGGACTTTTGATGG  
CCATGGGGTTTTCTTCTCCAACGGGGAGCGGTGGAGGCAGCTGAGGAAGTTTACCATGCTTGC  
TCTGCGGGACCTGGGCATGGGGAAGCGAGAAGGCGAGGAGCTGATCCAGGCGGAGGCCCGGTG  
TCTGGTGGAGACATTCAGGGGGACAGAAGGACGCCCATTCGATCCCTCCCTGCTGCTGGCCCA  
GGCCACCTCCAACGTAGTCTGCTCCCTCCTCTTTGGCCTCCGCTTCTCCTATGAGGATAAAGGA  
GTTCCAGGCCGTGGTCCGGGCAGCTGGTGGTACCCTGCTGGGAGTCACTCCAGGGGGGTCA  
GACCTACGAGATGTTCTCCTGGTTCTTGGCGCCCTGCCAGGGCCCCACAAGCAGCTCCTCCA  
CCACGTCAGCACCTTGGCTGCCCTTACAGTCCGGCAGGTGCAGCAGCACCAGGGGGAACCTGGA  
TGCTTCGGGCCCCGACGTGACCTTGTGCGATGCCCTTCCTGCTGAAGATGGCAGAGGGAACA  
AAACCCAGGACAGAAATTCACCAACAAGAACATGCTGATGACAGTCATTATTTGCTGTTTGC  
TGGGACGATACGCTGACGACACCGTCGCGCTATACCCCTCCTGCTGCTGATGAAATACCTCA  
TGTCCAAAAGTGGGTACGTGAGGAGCTGAATCGGGAGCTGGGGCTGGCCAGGCACCAAGCCT  
AGGGGAGCTTACCGCCTCCCTTACACCGACGCGGTTCTGTCATGAGGCGCAGCGGCTGCTGGC  
GGCTTCCCTGCCCCTTCTCCTTAGGGAAGCGTGTCTGCCTTGGAGAGGCTGGCCAAAGCGGA  
GCTCTTCTCTTCTTCCACCACATCCTACAAGCCTTCTCCTTGGAGAGCCGCTGCCCGCCGGA  
CACCTTGAGCCTCAAGCCACCGTCACTGGCCTTTTCAACATTTCCCCAGCCTTCCAGCTGCA  
AGTCCGTCCTCACTGACCTTCACTCCACCACGCAGACCAGATGAAGGAGGCAACTTGGAAAGTG  
GTGGGTGCCAGGACGGTGCCTCCAGCCTCAACAGTGGGCATGGACAGGGTTAATGTCTCCAG  
AGTGTACACTGCAGGCAGCCACATTTACACGCCCTGCAGTTGTTTTCCGGAGTCTGTCCCACGG  
CCCACAGCCTCACTTGACTCATGTGCTGAAGATGCACAACCGACACCCATACACAACCTACAA  
GGGCCACAAAGCACTGCTGGGTAGCTTTCCACAGACATAAATATAGTCCATCTGCAATCAC  
AAGCATATAGCCAGGTAACCCACCACTCCCTGGATCTGCAGCCCACACGTGGGAGTCTGGC  
TGTCACCTTACACAGCCACAGAAACGGCCACACATGTTTACAGCTCACAGCCCTCTCCATTC  
ATCGAATCTTCTAGTGTCTCTGTCCCTGGTGCCTGGCACAGGGAACAGCATGCCCCCTCCGGG  
GTCATGCCACCCAGAGACTGTGCTGTCTATGGCCCCAACTCATGCTCCCTCTCTGGCTACA  
CCACTCTCCAGCCTGTGACCCGATGTTCACACACCCCAACCTTGTGCCACAGCTAC  
CCACGTACAACATGTCCTGGCTCCCCAGAGTATCTTCCCACTGAGACAGCCGCCCCACAG  
AGGCACAGTCCCCAGCCACCTCTGCAACTGCAGCCCTCAGTCACCCCTTTTAAAGCACCTGA  
TTCTACCAAATGCAACACATCTGGGTCTGCGATTATGCACAGAGACTTTGGACATACGAGGA  
CCCTCAGACCGGAGGAACACCTGCCCAACCCCAACACGTGCTTATGTAACCACTGGAAAGCG  
GCCCTGCTGCCCCCTCCACACACATACACTCACTGATCTACAGCCCTGTTGGCGCTCA  
GAGTCCCACTAGACCAGTGGGAAGGGTTAGAGACCAAGTAGGGGCCAGTTTCCAATTACCC  
CTGTCAGGGAGTGAGCCGGATCTGACGTTCTCTTGACTTAAAGGTCGGCTTGGGAATTAA  
GTTTGTTTCTGGCCTTTAGCCTAAAAAAAAAAAAAAAAAAAA



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**FIGURE 64**

MEATGTWALLLALALLLLLTALSGTRARGHLPPGPTPLPLLGNLLQLRPGALYSGLMRLSKK  
YGPVFTTYLGPWRPVVVLVGQEAVREALGGQAEFSGRGTVMLEGTFDGHGVFFSNGERWRQ  
LRKFTMLALRDLGMGKREGELIQAEARCLVETFQGTTEGRPFDPSSLQAATSNVVCSSLFGL  
RFSYEDKEFQAVVRAAGGTL LGVSSQGGQTYEMFSWFLRPLPGPHKQLLHHVSTLAAFTVRQV  
QQHQGNLDASGPARDLVDAFLLKMAQEEQNPGTEFTNKNMLMTVIYLLFAGTMTVSTTVGYTL  
LLLMKYPHVQKWVREELNRELGAGQAPSLGDRTRLPYTDAVLHEAQRLLALVPMGIPRTLMRT  
TRFRGYTLPGQTEVFLLGSILHDPNIFKHPEEFNPDRFLDADGRFRKHEAFLPFLGKRVCL  
GEGLAKAELFLFFTILQAESLESPPDLSLKPTVSGLFNIPPAFQLQVRPTDLHSTTQTR

**Important features of the protein:****Signal peptide:**

amino acids 1-28

**Transmembrane domain:**

amino acids 294-313

**Glycosaminoglycan attachment site.**

amino acids 99-103

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 128-132

**N-myristoylation sites.**amino acids 51-57, 109-115, 115-121, 188-194, 207-213, 257-263,  
284-290, 339-345, 370-376, 444-450**Amidation sites.**

amino acids 140-144, 435-439

**Leucine zipper pattern.**

amino acids 32-54, 39-61

**Cytochrome P450 cysteine heme-iron ligand signature.**

amino acids 433-443

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**FIGURE 65**

CGGACGCGTGGGGCCGT**ATG**CGCGGCTCTGTGGAGTGCACCTGGGGTTGGGGGCACTGTGCC  
CCAGCCCCCTGCTCCTTTGGACTCTACTTCTGTTTGCAGCCCCATTGGCCTGCTGGGGGAGA  
AGACCGCCAGGTGTCTCTGGAGGTCATCCCTAACTGGCTGGGGCCCCCTGCAGAACTGCTTC  
ATATACGGGAGTGGGCACCAATTCCACACTGCACATATGTGTGGAGCAGCCTGGGGCCTCTGG  
CAGTGGTAATGGTGGCCACCAACACCCCCACAGCACCTGAGCATCAACTGGAGCCTCCTGC  
TATCCCCTGAGCCCCGATGGGGGCTGATGGTGCTCCCTAAGGACAGCATTCAAGTTTCTTCTG  
CCCTTGTTTTTACCAGGCTGCTTGAGTTTGACAGCACCAACGTCCTGATACGGCAGCAAAGC  
CTTTGGGAAGACCATATCCTCCATACTCCTTGGCCGATTCTCTTGGAACAACATCACTGATT  
CATTGGATCCTGCCACCTGAGTGCCACATTTCAGGGCCACCCCATGAACGACCCTACCAGGA  
CTTTTGCCAATGGCAGCCTGGCCTTCAGGGTCCAGGCCTTTTCCAGGTCCAGCCGACCAGCCC  
AACCCCTCGCCTCCTGCACACAGCAGACCTGTGACGTAGAGGTGGCCCTGATTGGAGCCT  
CTCCCGGGGAAACCGTTCCCTGTTTGGGCTGGAGGTAGCCACATTGGGCCAGGGCCCTGACT  
GCCCCCTCAATGCAGGAGCAGCACTCCATCGACGATGAATATGCACCGCCGCTCTTCCAGTTGG  
ACCAGCTACTGTGGGGCTCCCTCCCATCAGGCTTTGCACAGTGGCGACCAGTGGCTTACTCCC  
AGAAGCGGGGGGCGAGAATCAGCCCTGCCTGCCAAGCTTCCCTCTTCATCCTGCTTAG  
CATACTCTCTCCCCAGTCACCCATTGTCCGAGCCTTCTTTGGGTCCAGAATAACTTCTGTG  
CCTTCAATCTGACGTTTCGGGGCTTCCACAGGCCCTGGCTATTGGGACCAACACTACCTCAGCT  
GGTCGATGCTCCTGGGTGTGGGCTTCCCTCCAGTGGACGGCTTGTCCCCTAGTCTCTGGGCA  
TCATGGCAGTGGCCCTGGGTGCCCCAGGGCTCATGCTGCTAGGGGGCGGCTTGGTTCTGCTGC  
TGCACCACAAGAAGTACTCAGAGTACCAGTCCATAAA**TAA**GGCCCCGCTCTCTGGAGGGAAGG  
ACATTACTGAACCTGTCTTGCTGTGCCTCGAACTCTGGAGGTTGGAGCATCAAGTCCAGCC  
GGCCCCCTTCACTCCCCCATCTTGCTTTTCTGTGGAACCTCAGAGGCCAGCCTCGACTTCTTGG  
AGACCCCAAGTGGGGCTTCCCTTCATACTTTGTTGGGGGACTTTGGAGGCGGGCAGGGGACAG  
GGCTATTGATAAGGTCCCTTGGTGTTGCCCTTCTTGCACTCTCCACACATTTCCCTGGATGGG  
ACTTGCAGGCCTAAATGAGAGGCATTCTGACTGGTTGGCTGCCCTGGAAGGCAAGAAATAGA  
TTTATTTTTTTTCACAGGGAACCAAAAAAAAAA

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**FIGURE 66**

MRGSVECTWGWGHCA~~PS~~PLLLWTL~~LL~~FAAPFGLLG~~EK~~TRQVSLEVI~~PN~~WL~~G~~PLQ~~N~~LLH~~I~~RAVG  
TNSTLHYV~~W~~SS~~L~~GLAVVMVATNTPHSTLSIN~~W~~SL~~L~~SP~~E~~PDGGLMVL~~P~~KDSIQFSSALVFTR  
LLEFDSTNVSDTA~~A~~KPLGRPYPPYSLADFSWNNITDSLDPATLSATFQGH~~P~~MNDP~~T~~R~~T~~FANGS  
LAFRVQAFSRSSRPAQPPRLLHTADTCQLEVALIGASPRGN~~R~~SLFGL~~E~~VATL~~G~~QGPDCPSMQE  
QHSIDDEYAPAVFQLDQLLWGS~~L~~PSGFAQWRPVAYSQKPGGRESALPCQASPLHPALAYS~~L~~PQ  
SPIVRAFFGSQNNFC~~A~~FNLTFGASTGPGYWDQHYLSWSMLLGVGFPPVDGLSPLVLGIM~~A~~VAL  
GAPGLMLLGGGLVLLLHHKKYSEYQSIN

**N-glycosylation sites:**

amino acids 65-69, 95-99, 134-138, 159-163, 187-191, 230-234,  
333-337

**cAMP- and cGMP-dependent protein kinase phosphorylation site:**

amino acids 397-401

**Casein kinase II phosphorylation sites:**

amino acids 151-155, 249-253, 255-259

**N-myristoylation sites:**

amino acids 3-9, 63-69, 235-241, 273-279, 292-298, 324-330

**Leucine zipper pattern.**

amino acids 371-393

## FIGURE 67

CCGCGACGCGCGCTGAGGCCAACACATGCTGTATCTGCTTGGCGTATCTCCCTGCTTCCACGCGCGGT  
CTGGAGAGAGGGTTTACGCCGCCAGGACATTTACTGAGGTGGCGAATATTGGGAGCGCGCGATCGCTCCCTCTCG  
GGCCCTGTGTGTGTCTGGGCGCTTCTAGAGATGGCGGGATCTGACCCGAGCGTGCGCTCGGCTGGGAGACGAT  
CGCTCAACAGTTCGCGGCATCGCCTTACAAGAAGTTCCGTGAGGTCGCGGAGAGGATCGCTCCAAACGTGACAGC  
CTGTAGTCTGTGCGCGACAAGATGATCTGTGTCGCGCGGGGGCTTTCGCGACGTCACACAGTTCAGCTCGCT  
GTGGCTGGCGCAACATGAGTGGCGACCGTGGAGCGAGCGGCTGCGCTGCTGAGCTTCAGTCAAGAACCTTGGAT  
TCTGAGCGACAACTTATATTCAGCTTTCGTGGAGGACATCTGCGAACCTGAGCGCGCTGACGCTGCTCAAAT  
GAACACAAACGGCTCGGGCTCTGCTCCCGCGAGGACATTCGGTGGCTGACCGACCTGCGCTTCGCTGCGATCAA  
CAACACACCGCTGCGTAGCTCGGGCTGACACTTGAACGGCTTAGCGGCTGTACGCTTGTGCACTTATCACTA  
CAATCCCTTCCACTGCGGCTGCGGCTTGTGTGCTGCAAGGCTGGGCGCGGAGACCCGGGTGCTCTTACCCG  
GCCGACTCCATTTGCTGTGCTCGGCTCCGCGCTGCAAGGGGTGCGGTGTCGCTCCGCCCTCGCTTCGCT  
GCGACCGCCGAGGTGCATCTGAGTGGCGGACCGCTGTGAAGCACGTGACACGCCCACTGCGCGAGGACTGGG  
TGTCTGTGTTAGCACTGCATCTGAGCGCGGCCCACTACGCTTCGCTGCAATGGCAACTTCAGATTCGCCGTGGGCG  
CGTAGTCTTAGACCGACCCGGTCTGAGCGGGGAGGACGACGGGTGTTGGGCGGGAGGAAGGAGGAGGAGGAA  
TGGGGATTTGCTGACGCAAGCACGACCCAAACCGCGCACTCAGACACCGCTTGGCGCGCGCCCGCCAGCACCC  
CGGTTCTCTGGCGCTGCAAAATGGCTCCTTGTGTGGTCCCTCTGATGTGACAGGAGGGGGGCTGTACACTGT  
CCGTGCAACAAATGAGTCTGGGCGCAACTCTACGTCAATGACGCTGGGCGTGGGAGAGCCGGGCGCCCAAAC  
CGCGCTGGGCGCGGGGAGAACCCGACGACGACGCCGCCACTCTGAGGCGAAGTCCACAGCAAGGCGCGGG  
CAACACGCTCTCTGCTTCAAACCCGAGGCGAAATCAAAGGCGAAGGCTGGCCAGGTCAGCATTTCTCGGGGA  
GACCGAGACGAGCGCGAGGAGGACAAAGTGGGAGGAGGAGGCGAAGACAGATCTCTGCGGACCGCGCGGA  
CGAGACAGCTTGTGGACAGCGGGAGCCCTCTGCGTAGCTTTCAAACGACGCTTCAAACGAGCGCGAGAGTCAA  
CGCGCACTTCTTGAGCTTGGCGGTCACTCGGCTGTGATGTGGCGGAGCGGAGGCGGGGTGACAGCTCGGCT  
GGCTGCGCTCTGGGCGCTCGGGCGCGCGCGGCTGGCGGAGCCCGCGACCGCGGCGAGCCCTCGCGCTACT  
CTATCTGTGTTCCAGCGGGGCGCGCGCGGAGTCGAGTCAAGTTCGGTCCGCGTAGAGGAGGCGTCAACCGCTACGTGT  
TCGGGCGCTGCGCGGGGTACCAACTACTCCGATGTGCTGGCGCTGGCGCGGAGAGCTGCGACGTGCAAGTGT  
GTTTCTCCACAGAGAGGAGTCCCACTCGCTGTGTGTGATGCGGATGGGATGAGGCTATTCCTCTGTGTTCTGGCCAC  
AGTGGCCCTTCTGGGCGCGCTCTGCTCATCTGTGTGCTAAACCCGGGCAAGCTACGCTGCTGATCTCGCG  
GCTCGAGGCCCTCAACCTTATGGAGAAGGATCTGCGCGAGACTTCGACCCGCTGCTTGTACGTGAGTCCGA  
AAAAAGCTTACCGGCGAGCGCGGACGCGCGGCGGAGAGGAGCGACGACGCGAGGAGGAGGCTTATGAGAA  
CGCGGAGCAGGAGAGCCAAATGGGGACCTGCGACAGAGAGGAGAGGCTTGGCGGCTCTCACTGTGGAATCCCA  
GTCCAAAGCGCCACAGAGAGGAGCTCGAGCGGGCTCGAGTAGAGGATCTCGGCTCGGCTGGGCGCCGAGGCGGT  
CACACTCGCCACAGAGATTAATGGCACTACAGCGACAGCGGAGCTGAACATCGCGGCTCGGCGCGCCATT  
CCGCACTCCCACTTAGGTTGCTGGGAGGACGACGCTTAGGCTGGAGCAACTATGTCTCCGCGCTCCCAACCTCT  
ACCATACTCTCCCTCTTACTACTCCCAACTCTPACTACAGGAGGATCTATTAGGAGGTGGGCGGATTTACCA  
GTGCTCTTACCCACAGGCTGCATTTCTCTCGCGGGTGTAACTCCCTTCCCGCGAGCAGCAGTGTATTTACTTAC  
CCGATCGAAGACTCACCCGAGACGTGGGCGATATATGTCCCTCCATTCGCTCGGCGATTTACTTGGAAAT  
CCACCCCGCAGCCGCCCACTCGCTGGGCTCTGAGAGCAGAGGAAACGAGCGAAGACTTTGGAACACTCCGGGTA  
CGCGTGTCTTTCGGGCGCAGCCAGGACCGAGCTGGAGTCTGTGGGCTCCCACTGACCCCTCTCTCTCCCTTTC  
TTCTTTCTTTTTTTTATTTTAATTTTTATTTATTTATTTATTTATTTATTTTATTTTATTTTATTTTATTTGACGGAGTCTGGCTCTGCG  
CAGGCTGGAGTGCAGTGGCGGATCTGCGCTCACTGCATCTTCGCTCCCGGTTCAAGGATTTCCCTCTGCTCT  
AGCTCGCTAGTAGAGTGGGACTACAGGCGCGCGCACACGACCACTAATTTCTCTATTTTATGTAGAGACGG  
GGTTTCCACATGTTTGGCGAGGATGGTCTGATCTCTTGACCTAGGTGATGCATCTGCTCCGCTCTCAAAGT  
CTGGGATTAGAGCGCTGAGCGACCGCGCGGCCCTCTCCCTTTCAATCTCCTACTCCAGAGCGGGATTCG  
TGGCAACCCCTGATTTTATGTTCCAAAGCTCTCTCGCGGAGGGAACCAATTCCTTGTCTCTCCACCCGCCACC  
CCACTTCTGGGCACTGGAGTTCGAGCGCGGTGGCTGGGGCGGCTTTCAGCTCCGCGCTCAGATTTTCTGTTTCT  
GTGTTTCTCAAAGACGCGATTTTCGGGTTCTGGTGTCTAAACCCCTTCCAGCGCTCGGGAAGATCGAGTGTG  
TGTGTGGGGGGTAGGAGGGAATCGGTTTCTGTGCTCTCTCTCTAAATTAAGCGCGCGAGACGCGCGCG  
CCTTGGCGGCTGAGCTCTGGAATCTGTGTCGGGGCAATTTCTGTTCCGTGTGTGGGCTTTCGGAGTCTGT  
GCTCGCTCAACAGCGCCCTCCCGCGCTCCACCCACCCAGGCTTACGTGAAAGCGCGGAGCGGAGAGTCA  
GACTGTGGCCTCCGGGCTCGGGCTCTCTGGAGGGCTCGCGCCCTAGTTTCGCAAAAGCTGCTCGTGACTGTGCG  
GACTGTGCGACGGGATCCGATGGAGGCGAGCCCTCTGCTCTCGCTCTCGGCTCTCGGCTCGCGCCCGCCAC  
CGGCCCTCTTCTGGGCGGAATCTGTGTTCTGCGCGCTGTGATCGCTGACAGCGTGCTCTAGGAGAAATGCT  
TGTGCTCTGTAAGTGTGACCTGTGATGTGATGGGGGGCGGCGGGGGCGGAGCGGGGAGAGGAGGAGG  
GAGGGCGCGCGCGCGGACTCGGGCGGGGTTCTTTTTCATTTTGAAGAAAGCTCTGGGTTTGGCTGGG  
GGATTTTCACTCTCGGGATGAGCCCTCTCTCGGAGAGCGAGCACGCGGGGCTGGGAGCGAGATGACCCCC  
GCGCGCGCTGCCCTTTCTAAAGCGGTCTGGATTCAGTCAATAAACCAATCGGATTTGAA

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**FIGURE 68**

MEFLRALWLWVALLGVAGSCPEPCACVDKYAHQFADCAYPEGLPANVTTLSSLSANKI  
TVLRGAFADVTQVTSWLAHNEVRTVEPGALAVLSQLKNLDLSHNFISFFWSDLRNLSALQ  
LLKMNHNRLGSLPRDALGALPDLRSLRINNRLRTLAPGTFDALSALSHLQLYHNPFHCGCGL  
VWLQAWAASTRVSLPEPDSIACASPPALQGVPPVYRLPALPCAPPSVHLSAEPPEAPGTPLRA  
GLAFVLHCIADGHPTPRLQWQLQIPGGTVVLEPPVLSGEDDGVGAEEGEGEGDGLLTQTQAQ  
TPTPAPAWPAPPATPRFLALANGSLLVPLLSAKEAGVYTCRAHNELGANSTSIRVAVAATGPP  
KHAPGAGGEPDQGAPTSEKSTAKGRGNSVLPSKPEGKIKGQGLAKVSILETETETEPEEDTSE  
GEEAEDQILADPAEEQRCGNGDPSRYVSNHAFNQSAELKPHVFELGVIALDVAEREARVQLTP  
LAARWGPGGGAGGAPRGRRLRLLYLCPAGGGAAVQWSRVEEGVNAYWFRGLRPGTNYSCV  
LALAGEACHVQVVFSTKKELPSLLVIVAVSVFLLVLATVPLLGAACCHLLAKHPGKPYRLILR  
PQAPDPMEKRIAADFDPRASYLSEKSYAPAGGEAGGEEPEDVQGEGLDEDAEQGDPSGDLQRE  
ESLAACSLVESQSKANQEFEAGSEYSDRLPLGAEAVNIAQEIINGNYRQTAG

**Important features of the protein:****Signal peptide:**

amino acids 1-19

**Transmembrane domain:**

amino acids 587-610

**N-glycosylation sites.**

amino acids 52-55, 121-124, 337-340, 364-367, 474-477, 563-566

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 397-400

**Casein kinase II phosphorylation sites.**amino acids 19-23, 202-205, 289-292, 246-249, 411-414, 431-434,  
433-436, 440-443, 544-547, 583-586, 650-653, 700-703**N-myristoylation sites.**amino acids 15-20, 48-53, 165-170, 296-301, 351-356, 362-367,  
390-395, 419-424, 514-519, 536-541, 557-562, 561-566, 610-615,  
661-666, 716-721**Amidation site.**

amino acids 522-525

**Prokaryotic membrane lipoprotein lipid attachment sites.**

amino acids 10-20, 603-613

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**FIGURE 69**

GCGCGCGGGAGCAGCGAAGGGGGCGGCAGGGATCCTCCAGGCTGCCGGCTGGGAAGGCGTGGG  
 CGACCCGGTGTGTGGCGGCCAGAGCCCGCGTTTCAGCCCTAGGGAGGGAAGCCAGTTGAG  
 CGAAGTTCTCCATGAATGTACGTCACAAATGATGATGACCGACCAATCCCTCTGGAATCGCCA  
 CCATTGCTGAACGGAGAGGTAGCCATGATGCCCACTTGGTGATGGAGATCGAGCTCAGCAT  
 GTTATTCTCGTTCAAGTTAATCCAGGTGAGACTTTCACAATAAGAGCAGAGGATGGAACACTT  
 CAGTGCATTCAAGGACCTGCTGAAGTTCCCATGATGTCACCCCAATGGATCCATTCTCTCCATT  
 CATGTGCTCTCAGGTATATATCTCACAGGTGATTGAAGATAGTACTGGAGTCCGCGGGGTGGT  
 GTCACACCCAGTCTCCTGAGTGTTATCCCCAAGCTACCCCTCAGGCATGTCTCAACCCAT  
 CATCTCCCTCCCTATCTGACTCACCATCCACATTTTATTTCATAACTCACACACGGCTTACTAC  
 CCACCTGTTACCGGACCTGGAGATATGCCGCTCAGTTTTTCCCCAGCATCATCTTCCCCAC  
 ACAATATATGCTGAGCAAGAAATATACCATTTTATGGAATGTCAAGCTACATCAGCCGAGAA  
 GACCACTACAGCAAGCCCTCCGCACAAAAAATGAAAGACCGCCAGATCGATCGCCAGAACCCG  
 CTCACACGCCCTCCTTCTTCTATCTACAAAAGCAGCTGCACAAACAGTATACATGGCTATGGG  
 AAGGGCCATAGTGGTGGAAGTGGCGGAGGCGGCAGCGGTAGTGGTCCCGGAATTAAGAAAACA  
 GAGCGACGAGCAAGAGCAGCCCAAAGTGAATGATTACAGACTGCAAGAATATAGTTGGAA  
 GTAAAGAGGTGCAAGACATTTCTTCCGGGAATAGAGAAACACAGAGTTCTTAATATTACGGA  
 AGAGCAGTTGTGTTGCTCGGGTCCCCCTGTTGGACTTTCCTGTGGACCCACAGTGGTCTT  
 TCCTTCCCCCTACAGTTACGAGGTGGCCTTATCAGACAAAGGACGAGATGGAAAAATACAAGATA  
 ATTTACAGTGGAGAGAATTAGAATGTAACCTGAAAGATCTTAGACCCACACAGATTATCAT  
 GTGAGGGTGATGCCATGTACAATTCGTAAAGGGATCCTGCTCCGAGCCTGTTAGCTTCACC  
 ACCACAGCTGTGCACCCGAGTGTCTTTCCCCCTAAGCTGGCACATAGGAGCAAAAAGTCA  
 CTAACCTGCGAGTGGGAAGGCACCAATTGACAAACGGTTCAAAAATCACCAACTACTTTTAGAG  
 TGGGATGAGGGAATAAGAAATAGTGGTTTCAGACAGTGTCTTCTCGGGAGCCAGAAGCACTGC  
 AAGTTGACAAAGCTTTGTCCGGCAATGGGGTACACATTCAGGCTGGCCGCTCGAAACGACATT  
 GGCACCACTGGTTATAGCCAAGAGGTGGTGTGCTACACATTAGGAAATATCCCTCAGATGCC  
 TCTGCAACCAAGGCTGGTTCGAGCTGGCATCATATGGGTACGTTGCACTGGAGTAAGCCAGAA  
 GGCTGTTACCCCGAGGAAGTGATCACCTACACCTTGGAAATTCAGGAGGATGAAATGATAAC  
 CTTTTCACCCAAAATACACTGGAGAGGATTTAACCCTGACTGTGAAAAATCTCAAAGAGGC  
 ACACAGTATAAATTACAGCTGACTGCTTCTAATACGGAAGGAAAAAGCTGTCCACGCGAAGTT  
 CTTGTTGTACGACGAGTCTCTGACAGGCCTGGACCTCTACGACCGCTGTCTCAAGAGCCCA  
 GTTACATCTCATGGCTTTAGTGTCAAATGGGATCCCCCTAAGGACAATGGTGGTTCAGAAATC  
 CTCAGTACTTTGCTAGAGATTACTGATGGAATTTCTGAAGGTGAAGTTTGTGGCAATTTGTTT  
 ATTCAAATCCCAATAGCAAGCTCTGTTTTCTAATATAGTAAATGTCTTTATAGTAATAGTGA  
 AATCATTAATTTAAGATAGAATTATTATTAACAATAAACAACTTTAGTCACATATTGGCAG  
 TTTTTCTATTTCAAACACAGCACCCAGAGATCAGAGTCTACTTGAAACCTACATTTTGTGTTATT  
 TAACAATTTTTCTGTATCTTTTTTCATTGGTGTGTTTTGTTTTGTTATCTTTGTTTTGTTCT  
 TTGGTTTGGTTTGGTTTTGTTTTGTTTTTGGATACGATPCTCTGTACACAGGCTGGAGGGC  
 AGTGGCACAGACATGGCCCATTTTCAGTCTCAGACTCCTGGGCTTAAGTGACTCTTCTGCCACA  
 GAAGATGAGGAAGAAATACATTTTTCATAGTATGGGGTCTCACTATGTTATCTAGCTGGTCT  
 CAAACTCCTGGCCTCAAGCAACCCCTCCACCTTGGCCTCCCAAAGTGTGGGACTATAGACATG  
 AATCACCACTCAGCTTCCATGTCTTTTATGAAGTACAGGTTCTTAATTAATCAGATAAATT  
 TGGTATTTTCTATCTCCTAATGTCATATGTTTCTGGAAATCTTATAAGCAGCCGAGAGTG  
 TGGGCTCACGCTGTAGTCCCAGCACTTTGGGAGGCTGAGGTGGTGGTTCAGGAGATCAAGACC  
 ATCCTGGCCCAAGTGGTGAACCCCGTCTCTACTAAAAATACAAAAATAGCTGGGTGTGGTG  
 CGAGGCACCTGTATCCCACTACTTGGGAGGCTGAGGCAGAGAATGTCTTGAACCCGAGCAG  
 GCGGAGGTTGCACTGAGCTGAGATTGCACCCTGCACTCCAGCCTGGTGACAGATGAGACTC  
 TGCTCTCAAAAAAAAAA

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**FIGURE 70**

MMMTDQI PLELPPLLNGEVAMMHLVNGDAAQHVLVQVNPGETFTIRAEDGTLQCIQGPAEV  
 PMMSPNGSIPPIHVPPGYISQVIEDSTGVRVVVTPQSPECYPPSYPSAMSPTHLPPYLTHH  
 PHFIHNSHTAYYPVPTGPGDMPPQFFQHHLPHTIYGEQEIIIPFYGMSSYITREDQYSKPPHK  
 KLKDRQIDRQNRNLNSPPFSIYKSSCTTVYNGYGKGHSGSGSGSGSGPGIKKTERRARSSPK  
 SNDSDLQEYELEVVRQVDILSGIEKPQVSNIQARAVVLSWAPPVGLSCGPHSGLSFPYSYEVA  
 LSDKGRDGKYKIIYSGELEC NLKDLRPATDYHVRVYAMYN SVKGCSEPVSFTHSCAPECP  
 FFPKLAHRSSSLTLQWKAPIDNGSKITNYLLEWDEGKRNSGRQCFFGSQKHCKLTKLCPAM  
 GYTFRLAARNDIGTSGYSQEVVYCYTLGNIPQMPSAPRLVRAGITWVTLQWSKPEGCSPEEVIT  
 YTLEIQEDENDNLPHPKYTGEDLTCTVKNLKRSTQYKFRLTASNTEGKSCPSEVLVCTTSPDR  
 PGPPTRPLVKG PVTSHGFSVKWDPPKDNNGGSEILKYLLEITDGNSEGEVFGNCFIQIQ

**Important features of the protein:****N-glycosylation sites.**

amino acids 69-73, 254-258, 401-405

**Glycosaminoglycan attachment sites.**

amino acids 229-233, 234-238, 236-240

**cAMP- and cGMP-dependent protein kinase phosphorylation sites.**

amino acids 416-420, 535-539

**Tyrosine kinase phosphorylation site.**

amino acids 319-326

**N-myristoylation sites.**amino acids 52-58, 227-233, 228-234, 230-236, 231-237, 232-238,  
235-241, 239-245, 402-408, 610-616**Amidation site.**

amino acids 414-418

**Prokaryotic membrane lipoprotein lipid attachment site.**

amino acids 290-301

**ATP/GTP-binding site motif A (P-loop).**

amino acids 546-554

**CUB domain proteins profile.**

amino acids 294-301

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**FIGURE 71**

AAGTCATTAGTGGATGTGATCTTGCTCAGAGGGGACGATGCTCAAGCTCTTCTGGCTCCTTCTCAGCCTTGTT  
 GCTCTAACTGCTGCTCAGTCCACCATTTGAGGAACAGGCCAAGACATTTTGGACAAGTTTAAACCAAGAGCGCGAA  
 GACCTGTTCTTAAACAGTCTACTTGCTTCTGGAAATTATAACACCAATATTACTGAAGAGATGTCCAAACATG  
 AATTAATGCTGGGGACAAATGGCTGGCTTTTAAAGGAACAGTCCACACTTGCCCAATGTATCCACTCAAGAA  
 ATTCAAGATCTCAGAGTCAAGCTTCAGCTGCAAGCTCTCAGCAAAATGGGTCTTCAGTGCTCTCAGAAAGACAAG  
 AGCAAAACGGTTGAACACAAATCTAAATCAATGAGCACCATCTACAGTACTGAGAAAAGTTTGAACCCAGATAAT  
 CCACAAGAAATGCTTATTACTTGAACAGGTTTGAATGAATAATGGCAACAGTTTAGACTACAAATGAGAGGCTC  
 TGGGCTTGGGAAGCTGGAGATCTGAGGTGCGCAAGCAGCTGAGGCCATTATATGAAGAGTATGTGGCTTTGAAA  
 AATGAGATGGCAAGAGCAAAATCATTATGAGGACTATGGGGATTATTGGAGAGGAGACTATGAAGTAATGGGGTA  
 GATGGCTATGACTACAGCCGCGCCGCTTGATTGAAGATGTGGAACATACCTTTGAAGAGATTAAACCATTAAT  
 GAACATCTTCATGCCATATGTGAGGGCAAAAGTTGATGAATGCCATCCTTCCATATCAGTCCAAATGGATGCCCTC  
 CCTGCTCAATTTGCTTGGTGATATGTGGGGTAGATTTTGGACAATCTGTACTCTTTGACAGATCCCTTTGGACAG  
 AAGCAAAACATAGATGTTACTGATGAATGGTGGACCAGGCCCTGGGATGCACAGAGAAATTTCAAGGAGGCCGAG  
 AATCTCTTGTATCTGTTGGTCTTCCATTAATGACTCAAGGATTCTGGGAAAATTCATGACTCAACGGACCCAGGA  
 AATGTTCAAGAAAGCAGCTTCCCATCCACAGCTTTGGGACCTGGGGAAAGGGCAGCTTCAGGATCCTTATGTGCACA  
 AAGGTGACAATGGAGGACTCTCTGACAGCTCATCATGAGATGGGCGATATCCAGTATGATATGGCATATGCTGCA  
 CAACCTTTTCTGCTAAGAAATGGAGCTAATGAAGGATTCATGAAGCTTGTGGGGAATCATGTGCATTTCTGCA  
 TCCACACCTAAAGCAATTTAAATCCATTTGCTCTGTCAACCCGATTTTCAAGAGACAAATGAACACGAATTAAC  
 TCTGCTGCTCAACACAGCATCAGGATTTTGGGACTCTGCCATTTACTTACATGTAGAGAAGTGGAGGTGATG  
 GTCCTTTAAAGGGGAAATTTCCCAAGACCAAGTGGATGAAAAGTGGTGGGAGATGAAGCCAGAGATATGTTGGGGTG  
 GTGGAACTCTGGCCCATGATGAACACTACTGTGACCCCGCATCTCTGTTCCATGTTTCTGATGATTACTGATCTTC  
 ATTCGATATTACACAAAGACCTTTTACCAATTCAGTTTCAAGAGCAGCTTTGTCAGAGCAGTAAACATGAAGGC  
 CCTCTGCACAAATGTGACATCTCAAATCTACAGAAAGCTGGACAGAACTGTTTGAAGAAATACCTCAAATGTT  
 GAACCTCTCCTAGTATTGATATTACTCATTTCCATGCCAGGTTTGTATTTGATTTCTTTGTTCTTAAAGAA  
 ATTTATGCGCTCAAATGTCCCTATTACAAACCAACATTTAATTTCTGGTCAAGCAAGCAATGACCATTA  
 RACAAATGGGTGGGCCACCTCTTTCTCCCTATCATAACTACAGCCCTCTCTCTCGTAATTTGGAAGGAAAGAG  
 CGGTTTAGGGTGGAAATATATCTGTTAATATGATCTTTTCTTATCTGCCAGAGCAAAATTTAGCCAAAGTCAAAG  
 AGAAGAAACCATAGATCATAGATGTAAATATATGTACATCTGGAACCCCTCAAAGGGCCCTGAACCCCTTTT  
 TGTGTAGCAATATGCTGAGGCTTGGAAAATCAGAACCTGGACCCCTAGCATTTGGAATAATGTTGTAGGAGCAAGAA  
 CATGAATGTAAGGCCACTGCTCAACTACTTTGAGCCCTTATTTACCTGGCTGAAAGACCAAGAACTTCTTT  
 TGTGGGATGGAGTACCGACTGGAATCCATATGCAGACCCAAAGCATCAAAGTGAAGGATGAAGCTAAATCAGCTC  
 TTGGAGATAAGCATATGAATGGAACGACAAATGAATGTACCTGTTCCGATCATCTGTTGCATATGATATGATGAGGC  
 AGTACTTTTAAAGATTAATAATCAGATGATCTTTTGGGGAGGAGGATGTGCGAGTGGCTAATTTGAAACGAA  
 GAATCTCCTTTTAATTTCTTTGTCAGCTGCACCTAAATAATGTGTCATATCATCTCAGAACTGAAGTTGAAAAG  
 CCAACAGGATGTCCCGAGGCCGATCAATGATGCTTTCCGCTGATGATGACAAACGCTAGAGTTCTCTGGGATAC  
 AGCCACACACTGGACCTCTCAACACGCCCTCTGTTCCATATGGCTGATTTTGGAGTTGTGATGGGAGTGA  
 TAGTGGTGGCATTTGTCATCCTGATCTTCACTGGGATCAGAGATCGGAAGAGAAAATTAAGACAGAAAGTGGAG  
 AAAATCCTTATGCCCTCATCGATATTAGCAAGGAGAAATTAATCCAGGATTTCAAACACCTGATGATGTTCAGA  
 CCTCCTTTTGAAGAAATGATGTTTCTCTCTGAGTGATTTTGTGTGATGTAATTTAATTTTCAATGTTATAG  
 AAAATATAGATGATTAAGATATCATTAATGTCAAACTATGACTCTGTTTCAGCAAAAAAATTTGTCACAGACA  
 ACATGGCCCAAGGAGAGCATCTTCATGACATTTGTTTCAGTATTTATTTCGTCTCTGGAATTTGACTCTGTT  
 CTGTTCTTAATTAAGGATTTTGTATTAGAGTATATTAGGCAAGTGTGTATTTGGTCTCACAGGCTGTTCAAGGGA  
 TAACTCAATGTAAATGCTGTTGTAATTTCTGAAGTTGAAGAACAGGATATATTGAGCAAGATGTTCGATCT  
 TGTATGGAATTTGGAATGGATCACTTGAAGGACAGTGCCTGGGAAGTGGTGTAGCTGCAAGGATTTGAGATGGCA  
 TGCATAGCTCACTTTCAATTAATCATCTGCAAGGATGACATGCTTTCTCAGCATACTCAGTTCAAGTACTA  
 TGGTATTTGCCCTACAGTGATGTTTGAATCGATCATGCTTTCTTCAAGGTGACAGGCTTAAAGAGAGAAATC  
 CAGGGAACAGGTAGAGGACATGCTTTTCACTTCCAAAGTGCTTGATCAACATCTCCCTGACACACAACTA  
 GAGCCAGGGGCTCCGTGAACCTCCACAGGATGCTGATAGAACTGTTTACTGTTCTTCAATCTGTTGAGT  
 GAATGGAAATTTCAACTGTATGTTTCACTCTGAAGTGGGTACCCAGCTCTTAAATCTTTGTATTTGCTCACA  
 GTGTTTGGACAGTGTGCGAGCAACACAGACACATTAATGCTAGATTTACAAAA



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**FIGURE 72**

MSSSSWLLLSLVAVTAAQSTIEEQAKTFLDKFNHEAEDLFYQSSSLASWNYNTNITEENVQNMN  
NAGDKWSAFLKEQSTLAQMYPLQEIQNLTVKLQLQALQQNGSSVLSEDKSKRLNTILNTMSTI  
YSTGKVCNPDNPQECILLEPGLNEIMANSLDYNERLWAWESWRSEVGKQLRPLYEEYVVLKNE  
MARANHYEDYGDYWRGDYEVNGVDGYDYSRGQLIEDVEHTFEEIKPLYEHLHAYVRAKLMNAY  
PSYISPIGCLPAHLLGDMWGREFTNLYSLTVFPGQKPNIDVTDAMVDQAWDAQRIKFAEKFF  
VSVGLPNMTQGFWEWSMLTDPGNVQKAVCHPTAWDLGKGDFRILMCTKVTMDDFLTAHHMNGH  
IQYDMAYAAQPFLLRNGANEGFHEAVGEIMSLSAATPKHLKSLGLLSPDFQEDNETEINFLK  
QALTIVGTLFPFTYMLEKWRWMVFKGEIPKDQWMKKWEMKREIVGVVEPVPHDETYCDPASLF  
HVSDDYSFIRYYTRTLYQFQFQALCQAAKHEGPLHKCDISNSTEAGQKLL

**Important features of the protein:**

**Signal peptide:**

amino acids 1-17

**N-glycosylation sites.**

amino acids 53-57, 90-94, 103-107, 322-326, 432-438, 546-550

**N-myristoylation sites.**

amino acids 260-266, 286-292, 395-401

**Cell attachment sequence.**

amino acids 204-207

**Neutral zinc metallopeptidases, zinc-binding region signature.**

amino acids 371-381

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**FIGURE 73**

CCCACGCGTCCGAGCGGGGTGGACAAGTGGCGTGTGTGCTGCGACCCCGAGGGAAGATGAACG  
GGACGCGGAACCTGGTGTACCCTGGTGGACGTGCACCCAGAGGACCAGGCGGCGGCGGCGAGGA  
AGACCTATGCCATGGTGTCCAGCCACTCAGCTGGTCATTCTCTGGCTTCAGAACTGGTGGAGT  
CCCATGATGGACATGAGGAGATCATTAAAGGTGTAAGTGAAGGGGAGGTCTGGAGACAAGATGA  
TTCACGAGAAGAATATTAACAGCTGAAGAGTGAGGTCCAGTACATCCAGGAGGCCAGSAACT  
GCCTACAGAAGCTCCGGGAGGATATAAGTAGCAAGCTTGACAGGAACCTAGGAGATTCTCTCC  
ATCGACAGGAGATACAGGTGGTGTCTAGAAAAGCCAAATGGCTTTAGTCAGAGTCCCACAGCCC  
TGTACAGCAGCCACCTGAGGTGGACACCTGTATAAATGAGGATGTTGAGAGCTTGAGGAAGA  
CGGTGCAGSACTTGCTGGCCAAGCTTCAGGAGGCCAAGCGGCAACACAGTCAGACTGTGTGG  
CTTTTGAAGTGCACACTCAGCCGGTACCAGAGGGAAGCAGAACAAAGTAATGTGGCCCTTCAGA  
GAGAGGAGGACAGATGTCCAGAGTGAATTGGAGAATGTCTGGGGGAATGAAGTTCCTTCCACA  
AACACAGCTCAGTTCTTAGCAACAACTGTTTGTGTTTTCTACTTGCTCCATCTGCAGCCTACG  
CTGCCCTGGCCTCTCTGCAGACAGATAGTGGGGTTACCTGGCAAGGCCTGGTGAGAGCCAGTGA  
ACCTAAGCTTTGACTGGGTGGCCTTGCTTTTCTGGGGAGGAGGGAATGTACATTCAGGGAGTA  
GCCTTTTGGCGAAAAATTTCTTAGGGCTACAGACAGTCATGTGTGACTTCTCTCTGCTGTGAA  
AACTCCCAGAGTCTCTTTAGGGATTTCCCTAAGGTGTACCACCAGGCACACCTCAGTCTTCT  
TGACCAGAGCCTGAAAACCTGTTTCACTGGGTTCCACCAGTCCCAGCAAAATCCTCTTTGTA  
TTTATTTTGCTAAGTTATTGGTGGTTTTGCTTACATCTCATGATTGATATAATACCAAAGTTC  
TATAGCCTTCTCTTGCAGTATTGGGATTTGCTTGAAACCGGGAAACTGTTCCCATTAGGCTT  
GTTAATGTGAGAGTGACACTATTATGAATCTTCTCTCCCTTTCCTCTGCCTGTCTTCTCTCT  
CTTTCTCCTTCAAACCTTGCTCTGCAGCTAAGGAAGGTGAGTCTACTTCCCTGAGGCTTTGGG  
GTCAGAGTATATGTTGTTTGGAGAAAGAGGGCAATCAGGACTCTTCTGGGACCCAGATGAGTT  
CTTCACTAGCCCTTCTGAACCCCTTGCTCCATAAATGGTCTTTTATCCTGGCTCTGAATGACC  
CTGCAGGTCAFCATGGTTTCTTTTTTATGTTTTTTTTTTTTTCTGAGACAGAGTCTCACT  
CTGTACCCAGGCTGGAGTGCAGTGGCGCATCTCAGCTCACTGCAACCTCTGCCTCCCGGAT  
TTAAGCGATTCTTCTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGTGTGCCACCACGCCTG  
GCTGATTTTTGTATTTTAGTAGAGATGGGGTTTACCATACTGGCTAGGCTAGGCTCTCGAATT  
CCTGACCTCAGGTGATCCACCCACCTCGGCTTCCCAAAGTGCTAGGATTATAGGCTTGAGCTA  
CTGCGCCCGGCCATGGTGTTTTTCTTTAGGGCTCTTCTACAGCCTTGAGAAGTAGATAGGC  
ATCAGAGTATGGTACTATAGGAATCAGAAAAATTCAAAACAAATGTGGATTAAAGTGTATAGGC  
TCTATGTGGCTCACGCAGCCAGAATCCTTAAGTCTGTGTGTTTTCTGTGTCTCAAGACTGGGCT  
CACATTCTGGCTTTGTCCATAACAATGCTCTGGGATTTCAGGGAGTTCCCTCATTGTGAAAAAT  
GAGGGGGTCAGAGCAGGTGATATCCATGTTCTTCCCTTCTGATATTGTTGTCTGTGGCATA  
TTCTTTGTATGGCGAATTTAATAAAATATATTAATGTGTCA

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**FIGURE 74**

MNGTRNWCTLVDPHPEDQAAAGRKTYAMVSSHSAGHSLASELVESHGHEEIIKVYLKGRSGD  
KMIHEKNINQLKSEVQYIQEARNCLQKLREDISSKLDRLGDSLHRQEIQVVLEKPNQFSQSP  
TALYSSPPEVDTTCINEDVESLRKTVQDLLAKLQEAQRHQSDCVAFEVTLSTRYQREAEQSNVA  
LQREEDRCPE

**Important features of the protein:**

**Signal peptide:**

amino acids 1-39

**N-glycosylation site.**

amino acids 2-6

**Amidation site.**

amino acids 21-25

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**FIGURE 75**

GCTTGCACACATGGCTCCGGAGGCTCCGGTTGCCATCCGAGCCCTGCCAGGCTCTAAAGTTCCTCAACTGACAA  
CACCAGTAACCTAAATATAGGAGCAGTGGTGGGGACGGGCTGFCGACGGGCTCCTTTCACAGAGTCTCCGGACT  
GCAGATAAGGCTCAGGCCCCCTTTTGGTGAGAAAGCAGACAGCAGCTGGGGCTGGCGGACACCTGTGTCTGCATG  
CTGAAGAGATGGGTGAGCCGCTGGCCAGAGTAGCAAGGAAGGTCAACGAGACGGTGGAGAGCGGCTCTGACACT  
CTGGACCTGGCCGAGTCCAACTGGTCTCCTTTCCATTTGGCATCTACAAGTCTCCGGGANTGCTCTGGCCAG  
ATCCACCTCATCACCTGGCTTAACAACGAGCTTAAGTCCCTCACCAGCAAGTTCATGACCACATTCACTCAGCTC  
CGAGAGCTCCACCTGGAGGGGAACTTCCTACACCGCTCCCCAGCGAGGTGAGTGCCTGACGACCTCAAGGCC  
ATTGACCTGTCCCGGAACTTCAGGACTTCCTCAGGAGCTTACCGCTCCGGCGCTGGAGACCATCAAC  
CTGGAGAGAACGAGATCGTAGATGTGCCCTGGAGAAGCTGGCCGCCATGCCAGCTTGGCGAGCATCAACCTC  
CGCTTCAACCCACTCAAGCCGAGGTGGCGGTGATCGCCCGCCCTCATCAAGTTTGACATGCTCATGTCTCCG  
GAAGCGCAAGAGCCCCCTACCTTAGGCCACCTTCCTCATGCCACCCAGCAAGGACAGAGGCCACAGGCGTG  
GAACCTGGGAAGGAGGGAGGCCATGGGAGGCCAAGCTGGGGGCTGGGGCGGGTGGCGCGAGCAGCACGTGG  
TGGGTGGGTGACGTGGTCTGGATAGATAGCTTACAGCAGTAGTGGGCTCTGGAATGCCAAGGGAAGAGGCCAA  
GGTGGGGCTCGACGCTGGACTCGGCACTCAGAGCTGCTGTGCAAACTCAGGCAAGTCTCCTGCGCTCTGAGC  
CTTGTCACTTGAAAAAACAGGACCCCTTTCCCTCCTTTGGGCTTCCTGGAGSTTTTAAAGCAGTACGTGCTCCCA  
AGTTACCTCCAGATCAGCAGGSCACAGGTGGGCATTGCGAGGTATTTCTGAGCCCCGCGGGTTTGAGGCTCTGT  
TTTTAGTGCTGAGAGCCAGTTGCTGCCCTGAGAAGAGAAGACAACCTCCATCTATTTATTGCTTCTCGAGAACTG  
ACCTGGATCGGCCCTCTGCGAGGCCACAGTCTTCAGTCTCTGTGTCCCTGGACTGGTGGGAACCTGAACTAGGAG  
TCTTGGGAGAGCTGTGGTGGGAATATGGGCTGGCACTGCTGCAGGSCAAGAACATTCATGTAGGAGCCCCAGGAC  
CANCANGCTGGGAATGGGAGCAAGTCAGCTCAGCTCTGTCTATTCGCCACAGTTAAACAATTTGGCGGGGTGGGAA  
GTCTGTAGTGTCTCCCTCCTCTAGCATCACTCCTGAGCTCGGGGAGAGGTGGGCCAGAGAACAGCAGAGTCACTT  
ACACCTGCAGCTCTTGTCTAAAGTGATTAGATGGCCACCTCACCAGTGTCCAGTCCAGCAGCAGCCCTGGCTGCC  
TTGTCACTGGCTCCTGGGGGCGAAGGCCATGTGSAACACGGGATTTGTAGCCAGCCAGCTCCCAGGCCAACGCC  
CAAGGCCCTGATGACTGGTCTTCTGTAGGCCCTCAACCTGGCATCTTAGGGTATGTCAGGCAACAGGCTGTACC  
AGCTGTCTGTGTTTCCAGGACATGAACTTTCAATGCTAAAACTGGGACATTACCAGCAAGTGGGAGTGGTTG  
GTCCTCCTACCAAGAGAGGGCTCGGGCTCTTGCTTCCCGAAGACCGCTGTGGCTTGAGAACTTGTACTGCTTGG  
TCCCTCAGGTATCTACCTCCACCTTCTCCTCATCTGTGGAGCAAGCCAACTCAGTGGCCAGACCCACCTGATC  
TGCATCTTTGTTTGTCTCCAGAGACACTGAGGCCACAGAGCTTGAGGCAAGCCAGGCGCTGCAAACTCCTGTGTG  
CCGTGGACGAGTGGCCACTTACTACTCTCAAGGCTAAGATGTTGAGAGCTCAGACCACTGCTCAGAGCAGTAAT  
CCCTGCTCAGAATGCTCCCACTTCCCTCGTCCCTGCCAGGTCTCTGTCTCTTTGGGAAGAACTGATAGGTGG  
GCCATTTGTTGGGCCATCACTGAGCGCTCAGTATCTCAAGAGACTCTGTTCTATCTGCTCGTATCCCAAAGCCCTGG  
TTGGTCAAACTCTGGGCAAGGGTTTTCAGGATGAGGAGGTCAAGACAGGATGTCAGAGCTACCGAGTTTCATCT  
GTGGGTGTGGGGCAAGTGGGGCTGAAGTCTGTGAGGCTCGCTGCGCCACCTGCCTTTGTGCTTGGAGT  
GGGTTTCTCCTTTGTGAGAAGAGGCATCCTTCTCTGATGTGCACAAACACAATGTATGACCAGAGCCTTGCAA  
CTCAAACTGTGGTCTGTGGACAGCAGCGGCAGTGACACTGGGAGCTTGATAGGAATGCAGAGCTTAGGCCTCA  
CCCTATACCTCCCGACTCAGACCTGCACTTTAGCAAGACCCCAAGCTGATTCTATAGCACTTAGAGTTTGA  
AGCAACAGGACATAGGCTGGGGATGCTCCCGAGCAGAGGTGAAGTTTCTCTCAGTCTCTCCTCCCTGCCACTTCC  
AGGACTCTGAGCTGTGTTCAGGCTCCTCCCTAACCCAGCTGGGAGACACTGGGCTGTATAGTTGTTCCAGAG  
TCTGCATGGCACTCTCGAAGAGGGGTGTGACCTGCACCCAGGAGATGAGGTTTGGTGTGGCCAGCCCTC  
CAGACCGCGCTTCTGTGTTAAACCTCTGCATGCCAAGCTGCCTGTGCCCAAGTCTCCTACCTCAGGCTTTGAA  
GGGCGAGCTCTGGAAGTTGTTTCTCCTCTGCTGGAGAGTTGCCCTTGTCTGTCTTGGAAAGTGTGGGCGAC  
CACAGATGCCCCCAATCAGAGCTCAGAGTGAAGTGAAGCTTAAGCTTCAGTCTGCAATAAAGAAATGCATTGGTT  
TCAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA

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**FIGURE 76**

MLKKMGAEAVARVARKVNETVESGSDTLDLAECKLVSFPIGIYKVLNRNVSGQIHLITLANNELK  
SLTSKEMTTFSQLRELHLEGNFLHRLPSEVSALQHLK AIDLSRNQFQDFPEQLTALPALETIN  
LEENEIVDVPVEKLAAMPALRSINLRFNPLNAEVRVIAPPLIKFDMLMSPEGARAPLP

**Important features of the protein:**

**N-glycosylation sites.**

amino acids 17-21, 47-51

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**FIGURE 77**

CACCAACAAGCAATCGTTCATGAGAAAGCCGTGCACCCGCTGCAGTTGGGCCATGTGGTCCGCATCGTATTCAC  
 TAGTCCCCATTTGTACACCAAGTACTGTCCCGGGCGTCTCCAGCAGATGCCTGGAGCCTTCCACCTTCTCAAGCAG  
 GGTGGTGTGAGTGGCGTGTCTTCTCTCTCCGCTGGACCGGAGCCGTCCGGCGGAGCGACCCCGGGGGTGGAGAA  
 AAACCCGGCTTGGCTCGGAGGTGGTCTCGGCCCCCGGCCACCGCATCCCTCCCTCCAGAGGCGGGCGGC  
 GGCTCCCGGGCAGCGACGGCAGCAAGCAAGTGAAGCGGATGCTCCAGAGCTGCTTTTGTCTCGGTGAGCA  
 ATGGCTGAGCTGGTACATCTCGCTCTCCAGGTAGGAGATCTCCCGGGCGCTCTATGAATGCCGCTAGTTCTG  
 GTAGAGTGTGGCCTTCAGGTTCTGCGCGGTCTCTCCGCGAGCGCTGGATGGCGTGCCTGGTCTCTGAGGTG  
 CCGGTCCCATCCGACTGCTGCGAGAGTGTCTTACGATACAGCCGCGCTCAAAACCCCTGACTCCAGTTCGCG  
 ACGCAGCGCGGTCTCGCCCACTGTCCGAGATCGCCATCGCCATTCTCTCCGGGTCTCAGCGACTCACTGTCACTA  
 TCGCGCGCGCAGCGCCCGGGGTGTCTAGACCCACCCAAAGGCCAACCGAGCTCCTGGGCTGAGGAAGCAGGAATG  
 GGAACGAGACGAGTACGCTGCGCGGGTCTGAGCGTCAGACATCGCGCTGCGCAAGTGGGCGGAGCGCAGACA  
 TTGCGCTCGCGCAGCAATGCCATCGGTTAAAGCGCATGCGCAAGATGAGCTATTGCGGAAGTGAGGGGAGGAGAG  
 GCGCGAGAGAAATTCGGTACTCGCATGAACCGAGCGTGACGTTGAGGTTGAAATAACCGGCAAGAGTAAAG  
 GCTGAAACTAGCTTCTCGTAAAGCTTCGTAGGGCCGAGCCCTGTGAGCCAGGTTCTGCGGCCACTAGGAGGTGT  
 CATGCTGACTGCTTTTTTAAAGCCCTAGAATCCTTGGCTTCGGCGTTGGGGTAAAGTTCGCTCTCGTTCTCAA  
 GCGCGTTTCCGCGAATCTCGCGGGATTGACGGGCGCTCTCAGAGCCGCGCATCTCTAGGAGCTAGTCTGGTC  
 CTCGGCTAGCGGGCTTGGGTTCGCGCGTAACTGGGAGGCCAGCCTGACGCGCGGAGCCCGCTGTGATCCTGTC  
 GCACCAAGTATGATGATGATGTTGGCATCTCGGCTTCAGGAGGATGGAAGTTCGAGAGGCGGAGCGCGAT  
 CAGTCCCGAGGATCCCTGCTGCTGATGGACGCTCTGGGAGTTGGTGAGCCCAACCGAGTTCGAGGCACTG  
 TTTGTTCACTTTAAGCAGCAATTCCTCTGGGGCCAGCTGGAGGCGCTCGAGGTGAGGTGGAGCGTGCAGATGACC  
 CTGTGCTGTGGGATATGACCATTTAGAAGGAGGGGTGGAATGTTCATCCGCTCAGCGCAACCCCTTTTGAAG  
 TTGAGGCCAAGAAAGGATCTTTAGAGACCCCTCTGCATGAAATGATACATGCTATTATTGTTCACTAATAAC  
 GACAAAGACCGAGAAGGGCATGGTCCAGAATTTGTAAACATATGCATCGCATCAACGACCTGACTGGAGCCAT  
 ATAACGGTATACCATACTTTTACGATGAGGTGGATGAGTATCGCGCACTGGTGGCGCTGCAATGGGCGCTGC  
 CAGCACAGGCCACCTATTACGCTATGTCAACACRGCTACTAACAGGGAACCTCTGCTCATGACTATTGGTGG  
 GCTGAGCACCAGAAACCTGTGGAGGCACCTTACATAAAATCAAGGAACAGAGAATTACTCAAAAAGAGCRAA  
 GGAAGGCAAACTAGGAAGGAACAGTATTTGGCGCAGAGAATAAAGGTACCTTCGTGATATTCTTCTGATT  
 TTTATCTGACCATAGCTATGATGAAGACAAATACTGTCTTCAGAGAACCTGGTATTAGATAAACTTAAAGATC  
 GTTCTCGGTGTAGAAGTCTCAAGTGTAGACTTAAGCAAAAATCCCCTGTCATGAAATGATGGTAGGAAAC  
 AGACTTGTCTGTGACAGAAGTAAAGTAAAGTAGGAATAGTTCCATGGATATTTTATTTTTTAACTTTTTT  
 CAGTTCTTTTATTCAAAGAAACAAATCAATCTCTGATATATTTGAGGTAAAGTTCCTTTCCTATCTTGA  
 CTCACTGAGTTATTAGGAAACAGAGGCAAAAGATTGTCAAATAAAACAAATAATCAAGTAAACATGCCGG  
 AATATAGCTCTTAACATACACCCCTTCCATCAGCTGGATTCTATCCAAGTGAATCTATTGAGTATGATGTTGTTCA  
 TCAAAGATGGGAAAGGATATGACATATTTTGGCAGTACTTCATCTTCAAGATTACCCCTTTTCTGTGAAG  
 TTCAGAGTTACTGAAGTGTCTTCTTCTTGGGAAGTGTGTGACCCAAGAACATAGGTTATATTTCCCAATCTT  
 TAATATTGAGTGAAGAGCTATAGATGAATGTATGGAAGACCGTATCTTCAATTTCTGTGAGTAGAAGAA  
 GATAAGAAATGGGACAGAGTTTTCCTCCGGAATTACACATAAAGGACACTAAGCAATTTTCAAGGTAAATGT  
 TGCTCTGTGTGTGTGCTTTGGCATGATAAGATTCTTTATTAATATGAGAGAAATTTTTTTATCTTTATATT  
 CTCTCAATATCAGAACTCCGTAATCTGAAGATTGGCCCTCCCTCCATTAATAGGATGTATGGATGTAAGTGA  
 ATAAATACTAGTCTCTCATTTTGGAGAAACGTACATAGTTTAAATGTTTGTACTGTATTTCTTTGAGTTGA  
 GGCATCTACATAACCAATCTCTTTGCTTTTTTGGCAGATAAACCCCAAGAGGCTGAGGCCAGTGAATATCCCT  
 TTTAGTGGGAAAGGATATGTTCTAGGAGAAACAGCAATTTACCTTCACTTGGGAAACATGATCACTTCAATGCG  
 TTTATATAAACCAAGATCTTTTAAATCAAAACCATTCAGCAAAATGCTGTAGAACCTAATTTCTAAATCAAGGTG  
 AAATTTGAACAGAAATGTTTCAGTAAAAATTTCTCATCTGGTCTCCCTGCTGTGTAGTACAGTCAACCAATGTT  
 CTAAAGCAACTCTTCTAGAGTATCTTTCGCAACCAAAAGCCTTCAGAGGTGTGAATGGATCTCCAAGGATA  
 AGTGTAAAGTGTGGCAACATCCCTAAAACTCAGTCTCTTAGTTCTCAGAGAAGGTTTCACTCTCTAAGATA  
 TCCCTTCAAGAAATCTTCAAAAGTAACGGAATCAGCATCTGTGATGCCATCCCGAGATGTGAGTGGGTCTGAGAT  
 ACATTTCCCAAAATAACGCACTAGGCTAGAAGATAAAAAA

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**FIGURE 78**

MDDDLMLALRLQEENLQEAERDHAQESLSLVDASWELVDPTDQLQALFVQFNDQFFWGQLEA  
VEVKWSVRMTLCAGICSYEGKGMCSIRLSEPLLKLRPRKDLVETLLHEMIHAYLFVTNNDKD  
REGHGPEFCCKHMRINSLTGANITVYHTFHDEVDEYRRHWWRCNGPCQHRPPYYGYVKRATNR  
EPSADYWWAEHQKTCGGTYIKIKEPENYSKKGKGKAKLGKEPVLAAENKGTFFVYILLIFM

**Important features of the protein:**

**Signal peptide:**

amino acids 1-41

**N-glycosylation sites.**

amino acids 148-151, 217-220

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 184-187

**Casein kinase II phosphorylation sites.**

amino acids 30-33, 121-124, 154-157, 187-190, 192-195

**Tyrosine kinase phosphorylation site.**

amino acids 211-218

**N-myristoylation sites.**

amino acids 59-64, 85-90, 146-151

**Neutral zinc metallopeptidases, zinc-binding region signature.**

amino acids 108-117

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**FIGURE 79**

CGGACGCGTGGGTGGCAACCAGGAGAAGCCAAACTTGGTCCCCGGCTCGCGGAGTGCCTGCG  
AGCGGTGCTC**ATG**CGCGCTCTATGAGGTCTTCTCTCACCCGGTCGAGCGCAGTTACCGCGCGGG  
GCTCTGCTCCAAAGCCGCGCTGTCTCTGCTGCTGGCCGCTGCGCTCAGTACATCCCGCGCGCT  
GCTGGTGGCCCTTCGGAGCCACGGGTTTGGCTGAAGCGGAGCAGTACCGAGGAGACGCCGAC  
CGTGGCGCTTCCAACACCAGGTGCTGCTCGTGGCCCCGCTCGGACCCGAAAGCGACGGGTTCCCT  
CGCCTGGAGACCGTTCCCGCGCTTCAACCGGCTGCAAGGGGATCGCCTGCGCGTCCCGCTCGT  
TTCGACTAGAGAAGAAGACGAGAACCGAGGATGGGAAGACGGACATGTTACATTTTAAGCTGGA  
GCTTCCCTCGAGTCCACGGAGCACGTTCTCGGTGTCAGCTCATCCTGACTTTCTCCTATCG  
ATTACACAGGATGGCGACCTCGTGATGTCAGAGCATGGCGTTTCTCCAGTCCCTCTTCTCTGT  
CCCGGGATCCGAGTTATACGTGAACGGAGACCTGAGGCTGCAGCAGAAGCAGCCGCTGAGCTG  
TGGTGGCCTAGATGCCCCATACAACATATCCGTGATCAACGGGACCAGCCCCCTTTGCCTATGA  
CTACGACCTCACCCATATTGTTGCTGCCACAGGAGAGGAACGTTACACCGTCCCTGAATGA  
TCCCAACCCCATCTGGCTGGTGGGACGGGCCGAGATGCTCCATTTGTGATTAATGCTATCAT  
CCGATACCCGTGGAAGTCATTTCTTATCAGCCAGGATTCTGGGAGATGGTAAAGTTCGCCCTG  
GGTACAGTATGTCAGCATCTCTGTTATCTTCTCTGGGTGTTGAAAGAAATCAAGATCTTCGT  
GTTTCGAATCAGTGGTGGTGAACCCATTCCCTGTGACAGTGAAGCCCGGGAGCATGTGTAA  
GGAGCACTTATCC**TAGA**AAGGCCATTTCTGAAGACTCAGCAGGACCGTGGCTGCCTCATTTGTC  
ATCTTCTGGGAACATCTTAGGACCTTTTGAAGAGCCACAGCGGACACCTGCGGGCTTGTGTGC  
TTTTCCCTCAGACACAACCGTTCTTTCCGGTTTGTCTACACAGTTCGATATCTTCAGAGCT  
CCTGCAGAAATGTCAGGGACTAGTTTGTGAAGAGTCTGAGAGTTCCTGGAGGCTATAATTAG  
CTTTTGGGTTTTCCTCTTTGGCTTAGCGTTGAATTTTCAGGAGAAAATTCAGTCAGTTCAG  
ACATCTTGGAAAGAGTCCCATCTCTGGTCAAGCAGAGACTTTCCCTGTTGAATCAGGGAAC  
ACACTGTGCATTTCTTCTTCTGTTGTGAGCCACTCTTACTCTTTTCAGGGCTCTCTTGTGAC  
AAACATGCCAATCACTAGCACTTTGCACCCCTGGGCTTCTCCATTTCCCATTCACAGCTTTGA  
TTTCCAGAGCTGAGGCCTTAACTGGAGACCTGGAGGGGCAAGGCCCAAGGGCAAGGCCGCA  
TTAGCACAGGCAATCAGGAGGGGCCGCTGAAGGACACTTGGACCGTCCACCTGCCCCAGCCCA  
ACAGTCAGTCATCTGTATCAGCTCAGCTGAGCAGCCCTGGATCTTTGCCGTACTGTGACTGG  
GCTCTTTGCCCTATTTTCCCTCTGTCTGTGCCCTGGATGGCAGGCTGAAGTCAGAGGGGCT  
GTTTCATTCTCAGCCCCCTCAGCAGCACTGGGGGAAGAAAGCATTGTCAACACAGGTTCTTTC  
TGGCCCTCACCAACAGCCTGGGCATTTGGCCCTCCTCCTCCTTGACAGCCCTCCCCCTCCT  
GCAAAAGGACAGGGGGCAGCGGGTGGTGTGGGATGGCTGGCTGCCCTGACCAACACAG  
TTTATTTGGAAGGCTAGCGGGAAGCCAGCGGCTGGCGTTCCCTTGACTAAGGAACAGGGTG  
CCCATCAGAGTGGGCGGGCAGCTTTGGGAAGGACACAAGAAGCAGTAAGAGTGTAAGAGGA  
TGCCTGGCTGGGCGAGCCAGTCAGCCTGGCCACTAGCAGAATACCAAGCACTCCAGTGGATT  
ACCCTCGTGGCTAAGCAAGTGTCTGCAGGAGCAGAGATGGCTGGAAGGGGCTCTGCACACGG  
AAGATGGCTTTCTCAGCCCATCACCTCCTGAGGATGTGGGCGAGTCTCCTCCAAGACACATG  
GAGTGCTTCTTGTATCCCAAGAGGTCATTGCCACTGGAAGGACATGCCCGGCTGATCGAATG  
CTTCATGCCACCCAGAAACACACCCCTCAGTGTGTGCCTCAGTTACTTTGAGAGTCAGTTG  
TCGTTTTTAGTGCTCCTTTAGGCTTACTAAACAGTTTTTGGAAACAAGCTATTTTGAAGTAT  
TCAAGCAGAGGAATTCCTTAACACTGACCCCTTGCTTTTAAATATTCAGGCTGTTTAT  
ATGCCTAAATTTTTTCTTAAGATCTAAACGAAAATAGTTTCTTGTAAATTCACATAAGG  
CAATGAGATATGGAAGATGACAAGATACGTATAAACATTGGTTGCATCTTATTAATTAATT  
CTAATGCAAAATCTGTATAAAGAACCATGATGTTTGTAACTTCTAATTAATAAGTTCAAA  
ATGAG



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**FIGURE 80**

MALYEVFSHPVERSYRAGLCSKAALFLLAAALTYIPLLVAFRSHGFWLKRSSYEEQPTVRF  
QHQVLLVALLGPESDGFLAWSTFFAFNRLQGDRLRVPLVSTREEDRNQDGKTDMLHFKLELPL  
QSTEHVLGVQLILTFSYRLHRMATLVMQSM AFLQSSFPVPGSQLYVNGDLRLQQKQPLSCGGL  
DARYNISVINGTSPFAYDYDLTHIVAAYQERNVTTLNDPNPIWLVGRAADAPFVINAIIRYP  
VEVISYQPGFWEWVKFAWVQYVSILLIFLWVFERIKIFVFQNVVTTIPVTVTPRGDLCKEHLs

**Important features of the protein:****Signal peptide:**

amino acids 1-34

**Transmembrane domain:**

amino acids 268-284

**N-glycosylation sites.**

amino acids 194-198, 199-203, 221-225

**cAMP- and cGMP-dependent protein kinase phosphorylation site.**

amino acids 51-55

**Tyrosine kinase phosphorylation site.**

amino acids 250-259

**N-myristoylation site.**

amino acids 187-193

**Cell attachment sequence.**

amino acids 307-310

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**FIGURE 81**

GCGGGGAGCTTCCCTG**ATGG**TGCCCGCGCCTCCGAGCCGGGGAGGAGCTGCCAGGGGCCAGCTGGGCAGGAGCCT  
 GGGTCCGCTGCTGCTGCTCTTGGCGTTGGGACACAGCTGGACCTACAGAGAGGAGCCGGAGGACGGCGACAGAGA  
 AATCTGCTCAGAGACAAAATTCGCGACGACTAAATACCCGCTGCTGAAGTCTTCAGGCGAGCTCCACACTGTGA  
 CAGGAAAAAGTCTCTCAAGAGGATATTAATTTGTTCTTGGACAATGCATCCACAGAAGATTACGACGTTTGTGCGGA  
 GCCTCCCTGTGAACAGCAGCTCCAGGCACACTTTGGCCGAGTGCTGTGATCTGTATCCGGGATACCGATATGA  
 CCGGGAGAGACACCGGAAGCGGGGAGAAGCCATAGTCTGTGGATATTGATGAGTGTGCCAGCAGCAATGGGACGCT  
 GTGTGCCCATCTGTCATCAATACCTTGGGCAGCTACCGCTGCGAGTGCCGGGAAGGCTACATCCGGGAAGATGA  
 TGGGAAGACATGTACCAGGGGAGACAAATATCCCAATGACACTGGCCATGAGAAGTCTGAGAACATGGTGAAGC  
 CGGAACCTTGCTGTGCCACATGCAAGGAGTTCTACAGATGAAGCAGACCGCTGTGTCAGCTGAAGCAAAAGATTGC  
 TCTGCTCCCAACAATGCAGCTGACCTGGGCAAGTATATCACTGGTGACAAGGTGCTGGCCCTCAAACACCTACCT  
 TCCAGGACCTCCCTGGCCTGCTGGGGCCAGGGCCCTCCCGGCTCACCAGGACCAAGGGAAGCCAGGCTTCCC  
 CGGTATGCCAGGCCCTCTGGGCAGCCGGGCCACGGGGCTCAATGGGACCCATGGGACCATCTCCTGTATCTGTC  
 CCACATTAAGCAAGGCCGGAGGGGCCCTGTGGTCCACCAGGGGCCACAGGAAGAGATGGTTCTAAGGGGGAGAG  
 AGGAGCGCTGGGCCCAAGGGTCTCCAGGACCCCTGGTTCTTCGACTTCTGCTACTTATGCTGGCTGCAT  
 CCGCAATGACATCACTGAGCTGCAGGAAAAGGTGTTGGGCACCGGACTCACTCTTCAGCAGAGGAGTTCCCTTT  
 ACCTCAGGAATTTCCCGACTACCCAGAAGCCATGGACCTGGGCTCTGGAGATGACCATCCAGAGAAGCTGAGAC  
 AAGAGACTTGAGAGCCCCAGAGACTTCTACC**ATAG**CACATCCCAACACCGTCAGCCAAAGGAAGAGAAAGAT  
 CAACTCACCTGCAGTTAAACCATCTAAAGAGAAAGAGACCACTGGAGACCTAGAAAACATACATTTTCTCTCT  
 TCTTCTCTGACGTCTCTCCACTCCCTCTCTTCCAAATACGATGCTATTTTCAGAGTCCCCCTCCTAGGCCCTGCAG  
 ACATGAGGGAGTGAATGATTGATTACCTGCTTCTCACTAAGAGTCCATTGGGGTGGTTGCATTGTAACTTTTC  
 TTTTACATCTCTATTTTCCAGGAACCTTTGGATTAAAGTACTCTCACAGTGTCTTAATATCAATAATCTTGAAGTT  
 AAATTTGGCAGAGTATCAAAAGGGGAAAAATGACAAAGTGAAGTCTAAGAAAATGTGAGGCTACTTCTAAGATGT  
 GTGTTCCAAATAGACATAACTCTCTAGTATCAAAATTTGGGCTCTTCAGTTAAAAGGGGTGGGAGGACAAA  
 CGTGTGATGTGCTTTGGTGGGAAGATTTTTCCTTGGCTTCTAGTAGACTTTAAATATTGATTCCTTTGTCAA  
 ACCTTGTTTCCCAATCTCAATTAAAGAGGAGAGAAATGAATGGCGTTTAGAGAAGATAGAAAAGAAATCAGAT  
 CATATATTACTGTTATATAGATTGGCCATCTCTAAAATTCAAATACGGTGCTTAAGGTTTCATGCCATGCTTAT  
 CTGTAAGTATCTCTATTAGGGAAGAAGATTAACCTCTCTTTTCAAAAAACAAAGTGAAATGCCCTGATTCACAT  
 TAAACAATGGGCTCTCGTTTGCTATAATATTTTAAAGCTGTTTAAATCAACAGTGGAGTCTGCTCTATAAATATA  
 GATTATTTGTTCAATAAAGTGGCTGAGCTTAGAGAGAGGTGCAGAAATTCCTGGTCTGAGCAGGTGCCAGAGG  
 TACCATTAGTGCCATGATCCAGGCTGAACCAATATACAGTGGGGCTGAAGTCTGCAAGGAGGTTGCTGGCTGG  
 GCTGACCTCACTAATGCCATCAGCAGCGGTAGGTAAATTTTTCTCCTTGGGTATTACAGTTTGTCTGGAGC  
 CAACCAAGCTTGCCACCAACATATTGAGAGTAATACACTATTGAAAGTTATCTTGGATGGGGAGAAAAAAATA  
 GTGGTTTTCTTGTTTGGCAAAAGTTCCCTTCTATCTCATTTTTCCTTAATTTCTTTAATTTAGTCCAGGTTT  
 CAGTTCTTTTAGGCTCTCTCTTTGATTTTATTTTCCCTGCAATGTGAGAAGCAGTTCAGAAAAAGGTCTATATCTC  
 CACCTCTACTGAGTTAGAGTGTCTTCTCAGAGCACCTCTGGGTGGCAAGGGAAGCATGTTCTCTGCCAGGTTT  
 GCTGTGGATTCAAGAGACCCAGGAGCAAGACCAAGAGATGATCTGCTCTTTTAAAGTTGTTAGGCTCTTGAAGGCCCT  
 CTGTTTCCAATGAGCAGCTTATAGGTTACTCAGAGTCCATTTCTCAGTCACACAAAGTGGCTCTTTATCT  
 ACCTTTTGGCGGAGATTTTCACTCTCTCGAAATGATGTTCTCACACTATATTAGTCATGTTGGATTTTCCCA  
 TCTCTGGCATGTTTCCCTATTTCTTTTGGCTTTTGGCTCCACCTTTTAGCCACACATCATTTAAGCTCCATCA  
 CTGTGAAGCTTGTCTTAAAGAAATCCCTCTTGGCGGGTGTGGTAGCCACCGCTCTAATCCAGCACTTTGGG  
 AGGCTGAGGCGGGGAGATCACAGGTCAGGAGATCGAGACAGGCTGACCAACATGTTGAACCTGCTCTACT  
 AAAAATACAAAATTAGCTGGGCGTGTGGCACACACTGTAATCCAGCTACTCAGGAGGCTGAGGCAGGAGAA  
 TTACTTTAACCTGCGGGGGAGCCTAGATTGCGCTACTGCACCTCAGCCTAGGCAACAGAGGGAGACTCTGCTC

ATTAAAAA

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**FIGURE 82**

MVPPPSRGGAARQQLGRSLGPLLLLLLALGHTWTYREEPEDGDREICSESKIATTKYPCLKSS  
GELTTCYRKCKCKGYKFVLGQCIPEDYDVCAEAPCEQQCTDNFGRVLCTCYPGYRYDRERHRK  
REKPYCLDIDECASSNGTLCAHICINTLGSYRCECREGYIREDDGKTCTRGDKYPNDTGHEKS  
ENMVKAGTCCATCKEFYQMKQTVLQKQKIALLPNNAADLGKYITGDKVLASNTYLPGPFGPLP  
GGQGGPPGSPGPKGSPGFPMPGPPGQPGPRGSMGPMGSPDLSHIKQGRRGFVGGPPGAPGRDG  
SKGERGAPGPRGSPGPPGFSFDLLLLMLADIRNDITELQEKVFGHRTHSSAEFFPLPQEFPSYP  
EAMDLSGSDDHPRRTETRDLRAPRDFYP

**Important features of the protein:****Signal peptide:**

amino acids 1-34

**N-glycosylation sites.**

amino acids 142-148, 182-188

**Tyrosine kinase phosphorylation site.**

amino acids 125-132

**N-myristoylation sites.**

amino acids 10-16, 143-149, 155-161, 196-202, 250-256

**Amidation site.**

amino acids 299-303

**Aspartic acid and asparagine hydroxylation site.**

amino acids 150-162

**Cell attachment sequence.**

amino acids 176-179

**Clq domain proteins.**

amino acids 247-280

**Calcium-binding EGF-like domain proteins pattern proteins.**

amino acids 144-165

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**FIGURE 83**

ATCTGAGTGAGCTAACTGACACAATGAACTGTCAGGCATGTTTCTGCTCCTCTCTCTGGCTC  
TTTTCTGCTTTTTAACAGGTGTCTTCAGTCAGGGAGGACAGGTTGACTGTGGTGAGTCCAGG  
ACCCCAAGGTCTACTGCACTCGGGAATCTAACCACACTGTGGCTCTGATGGCCAGACATATG  
GCAATAAATTGCCTTCTGTAAGGCCATAGTGAAAAGTGGTGGAAAGATTAGCCTAAAGCATC  
CTGGAAAATGCTTGAGTTAAAGCCAATGTTTCTTGGTGACTTGCCAGCTTTTGCAGCCTTCTTT  
TCTCACTTCTGCTTATACTTTTGCTGGTGGATTCTTTAATTCATAAAGACATACCTACTCTG  
CCTGGGTCTTGAGGAGTTCAATGTATGTCTATTTCTCTTGATTCACCTGTCAATAAAGTACATT  
TGCAAAAGCAAAA

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**FIGURE 84**

MKLSGMFLLLSLALFCFLTGVFSQGGQVDCGEFQDPKVYCTRESNPHCGSDGQTYGNKCAFCCK  
AIVKSGGKISLKHPGKC

**Important features of the protein:**

**Signal peptide:**

amino acids 1-23

**N-myristoylation sites.**

amino acids 26-32, 52-58, 56-62, 69-75

**Kazal serine protease inhibitors family signature.**

amino acids 40-63

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**FIGURE 85**

GGAGCAGACACACAGACCCGGGCCGGAGGCCCTCTTCTAGCCCTGCGGGAACCGGACAGTTCC  
CCCAACTGGGGACTCTGGAACCAACAGCTCCTAAATCATCAAATTTCTCAAGCTTTTTTTTTTCCC  
TCTCTTCGTCCCAGCCATCCCACTCTCTCTCTCTTTTTTTTTTTTTTAACCTATTGTTTTTT  
TCGCTCTCTGCATTATGAAAGTGGTCACGCCATTCAATATTAGACTTTGGAGGGAAATGGGGGA  
AAGAAAAGAAAGAAATCTAAAGAGAGAAGCGACCGGTGCTTTTAAGGGTGTCTAATTTTCAA  
AAGAGACGCTCGGGAGTATTTTGCTCTGGGCGTTTGGAGCAACTTCGCGGACAGCGGAGCTCG  
CCCAGCATGGATGTTCCAGGTTTACAGGCGCCTTCTTCTGAGAACGACCCCTGGCCTTGAACG  
TCAGAGCCGGGGAGGAAGGCCCCCGGAGGCTGCTGCGAGCTCCGCGCGTTCCCTCGCGCCTT  
CCGCGCGCTCGCGCCGGCGCGCGCCTCCACCCCGCGCGCGCCTCCCACAGTCCCGATGC  
AGGCGCCCGGCCGGGGGCCACTCGGGCTGCGGCTGATGATGCCGGGCGCGGGGGCGCTGC  
GCGAGCTTGGCGGCTGCGGATCTGCTTGGGGTGGCGCTGGCCCTGCTGTTGCTGCTACTGC  
CCGCCCTGCTGCCCGTGGCGGCGCAGAACGACACGGAGCCCATCGTCTGGAGGGCAAGTGCC  
TGGTGGTGTGCGACTCCAGCCCTCGCGGACGGCGCGTCACTCCTCCCTAGGCATCTCCG  
TGCGCTCCGCGAGCGCCAAGGTGGCCTTCTCCGCCACGCGGAGCACCAACCACGAGCCGCTCCG  
AGATGAGCAACCCGACCATGACCATCTATTTTCGACCAGGTATTAGTAATATTGGCAACCACT  
TTGATCTTGGCTTCAGTATTTTGTAGCACCGAGAAAAGGGATTATTAGCTTACGCTTCCAGC  
TGGTCAAAGTGTAACAGACAAACCATCCAGGTGAGTTAATGCAAGTGGCTACCCAGTGA  
TCTCGGCCTTTGCAGGAGACCAGGATGTCAACAGAGAAGCTGCTAGCAATGGCGTGCTGCTGC  
TCATGGAAAGGGAAGACAAAGTGCATCTCAAACCTTGAGAGAGGCAACCTCATGGGGGGCTGGA  
AATACTCCACATTTCTCGGGCTTCTTGGTGTTCCTCTATAAACACAGAGCCCCCTAGATGGTG  
GGGGAATGGCAAACCTGGACCCAGGACTCCGCCCTTTAAACACCCCTGAACCTTACTGGAATTGG  
ACACCTTGTTTCCAACTCCGTCAGACTGTTGCACTAGAAGATGATTTCCCTTTGAAACCTCC  
AGTACTTTTGTTTTGTTTTTGGAAATGACAATTCCTCGGGAACCTGGCCTCTAATTAGT  
TTTAGATGACAAGGTCTTAAGGAGAAATGAAATTATCGATTGAGCAATTTGTACCTGTGATT  
GTAAAGTCAATATCGGATTTTATTGTTGGGACCATGGACCTCTTTTGTGTTATGTTGATTG  
TCGTCCCAACGGAAGGAGAGCTCCTGACTCCAGGATGGGCTGCAAGTTGCACTGAGGGCTTGA  
AGTAGGAGCCAGCAAAGAACACCTGCTGGACAGTCCCTGACATGTGTTCTGTGTGTGCTGTG  
TATAGCCTTAAGAAAAAGAAATGGCTTCACTTTCATTCTGTATTTCCCCCAGCTTGGGCT  
GGGAGGACTTTGGGAGGGGGATGGGGACATTGGGAACCTGTCAAGAAGTGCTTTATCCAGAGAA  
GCAAATTTTGCACGATTTGAGCTGCAATTTTGTGTTGTATTTGTTGTTTCTTTGAAAG  
CTTTACTTTTTCCTCCACTCAGCTCCTCCCTCAACCCCACTTTATTTTCTTGTCTGGG  
GTTGAGGAGAGAAAAATATAGAATTCCTGGATAAGACCAACAAAACAAAACATTAATACCT  
GTATGTTTGTGTTTAGACGAGACCAAACTAAACAAAAGTATCTGTTTATCAAGTAAAGATA  
ACACAATGGCAAAATTCGCTTATCTCTCAAGAGATCTAAGATGCACCTTTAGAACTATTA  
ATAGCAACCTGCATTTTTTTTAATTTATACTTCAGAATCCTTTAAGAACCTGGGTCTCTCTGA  
GTGCTCTGAAATCATATAAGTTGGTAATGGAAGCTGTAATGACCAAGTCCCTTAACATACTA  
TGCTCTGCAACGCTGTGCTGTGACTTCTCTGTGGTGATTAAATTTATTTGGATCCACCTCTG  
AGTGAGCGCACAGGTATCAGGTGCTTCAAAGCCAAACAGACCAAGCTCCTCTTCTCCGGATCCT  
CTTTTGATCTGCCAGGAAGGATGCATTGACACTCTCTGATGCACCTGCGGAGGAAGCCA  
CCTGAAAGTCACTGTGGTTAAAGATATTGGTGGAGGTACCCAGGAGCACTGTTACAAATCCT  
TCTTGTTTTGGCATCTCTGACAAATATTAAAGACACAGCTGAGAGTTGATGGGTGTGTAATG  
CATATGCGAAGGAATGTCACTAATCCAAAGCAATCAAAAAGGAGACCTCAACCCAGATGTT  
AATTTGCTCTTTGTGTAACAATGTAAACCAAAATATTGATGATAAAAGTCATAATTTAAGATTC  
AGAATAAATGGGTTGATGCTCGGCAAAAAAAAAAAAAAAAAA

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**FIGURE 86**

MQAPGRGPLGLRLMMPGRRGALREPGGCGSCLGVALALLLLLLLPACCPVRAQNDTEFIVLEGK  
CLVVCDSPPSADGAVTSSLGISVRSGSAKVAFSATRSTNHEPSEMSNRTMTIYFDQVLVNIGN  
HFDLASSIFVAPRKGIYSFSFHVVKVYNRQTIQVSLMQNGYPVISAFAGDQDVTREASNGVL  
LLMEREDKVHLKLERGNLMGGWKYSTFSGFLVFPL

**Important features of the protein:****Signal peptide:**

amino acids 1-48

**N-glycosylation sites.**

amino acids 53-57, 110-114

**N-myristoylation sites.**

amino acids 26-32, 27-33, 29-35, 33-39, 76-82, 205-211

**Amidation site.**

amino acids 16-20

**Clq domain signature.**

amino acids 117-148

**Clq domain proteins.**

amino acids 115-149

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**FIGURE 87**

AGGGCCCGCGGGTGGAGAGAGCGACGCCGAGGGC**ATG**CGGGCAGCGTCCCGGAGCGCCTCTG  
GCTGGGCGCTACTGCTGCTGGTGGCACTTTGGCAGCAGCGCGCGCGGCTCCGGCGCTCTTCC  
AGCTGCAGCTGCAGGAGTTTCATCAACGAGCGCGCGTACTGGCCAGTGGGGCGGCCTTGGCAGC  
CCGGCTGCCGGACTTCTTCCGCGTCTGCCTTAAGCACTTCCAGGCGGTCTCTCGCCCGGAC  
CCTGCACCTTCGGGACCGTCTCCACGCCGGTATTGGGCACCAACTCCTTCGTGTCCGGGACG  
ACAGTAGCGCGGGGGGCGCAACCCCTCTCCAACCTGCCCTTCAATTTACCTGGCCGGGTACCT  
TCTCGCTCATCATCGAAGCTTGGCACGCGCCAGGAGACGACCTGCGGCCAGAGGCCCTTGCCAC  
CAGATGCACTCATCAGCAAGATGCCATCCAGGGCTCCCTAGCTGTGGGTCAGAAGTGGTAT  
TGGATGAGCAAACGAGCACCCCTCACAGGCTGCGCTACTCTTACCGGCTCATCTGCAGTGACA  
ACTACTATGGAGACAACCTGCTCCCGCTGTGCAAGAAGCGCAATGACCACCTCGGCCACTATG  
TGTGCCAGCCAGATGGCAACTTGTCTGCTGCCCGGTGGACTGGGAATATTGCCAACAGC  
CTATCTGTCTTTCGGGCTGTGATGAACAGAAATGGCTACTGCAGCAAGCCAGCAGAGTGCCCTCT  
GCCGCCAGGCTGGCAGGGCCGGCTGTGTAACGAATGCATCCCCACAATGGCTGTGCCACG  
GCACCTGCAGCACTCCCTGGCAATGTAAGTGTGATGAGGGCTGGGAGGCCCTGTTTTGTGACC  
AAGATCTCAACTACTGCACCCACCACTCCCCATGCAAGAATGGGGCAACGTGCTCCAACAGTG  
GGCAGCGAAGCTACACCTGCACCTGTGCGCCAGGCTACACTGGTGTGGACTGTGAGCTGGAGC  
TCAGCGAGTGTGACAGCAACCCCTGTGCAATGGAGGCAGCTGTAAGGACCAGGAGGATGGCT  
ACCACTGCCCTGTGCTCCCGGCTACTATGGCCTGCACCTGTGAACACAGCACCTTGAGCTGCG  
CTGGATTACGGGCACCTACTGTGAACCTCCAGTCAAGCTGAGCTGAGCTGGAGC  
GTGAATGTCCCCCAACTTCACCGGCTCCAAGTGCAGAGAAAGTGGACAGGTGCACACAGCA  
ACCCCTGTGCCAACGGGGGACAGTGCCTGAACCGAGGTCCAAGCCGATGTGCCGCTGCCGCT  
CCAGCTCCCCCTGCTTCAATGGGGGCTCCTGCCGGGAGCGCAACAGGGGGGCCAACTATGCTT  
GTGAATGTCCCCCAACTTCACCGGCTCCAAGTGCAGAGAAAGTGGACAGGTGCACACAGCA  
ACCCCTGTGCCAACGGGGGACAGTGCCTGAACCGAGGTCCAAGCCGATGTGCCGCTGCCGCT  
GCGAGCGCTGTGAGGTGCGGACATCCATCGATGCTGTGCCCTCGAGTCCCTGCTTCAACAGGG  
CCACCTGCTACACCGACCTCTCCACAGACACCTTTGTGTGCAACTGCCCTTATGGCTTTGTGG  
GCAGCCGCTGCGAGTTCCCCGTGGGCTTGCCGCCAGCTTCCCTGGGTGGCCGCTCTCGCTGG  
GTGTGGGGCTGGCAGTGCTGCTGCTACTGCTGGGCATGGTGGCAGTGGCTGTGCGGCAGCTGC  
GGCTTCGACGGCCGGACGACGGCAGCAGGGAAGCCATGAACAACCTTGTGGACTTCCAGAAGG  
ACAACCTGATTCTCGCGCCAGCTTAAAAACACAAACCAGAGAAGGAGCTGGAAGTGGACT  
GTGGCTTGGAACAAGTCCAAGTGTGGCAACAGCAAAACCACACATTGGACTATAATCTGGCCC  
CAGGCCCTTGGGGCGGGGGACCATGCCAGGAAAGTTTCCCCAGTGACAAAGAGCTTAGGAG  
AGAAGGCGCCACTGCGGTACACAGTGAAAGCCAGAGTGTCCGATATCAGCGATATGCTCCC  
CCAGGAGTCCATGTACAGTCTGTGTGTTTGATATCAGAGAGAGGAATGAATGTGCTATTG  
CCAGGAGGTAT**TA**AGGCAAGGACCTACCTGGACATCCCTGCTCAGCCCCGCGGCTGGACCTTC  
CTTCTGCATTGTTTTACA